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ccaacacagg	acaagatggt	gtctgtatcc	tacaccatcc	tcactccc		648

&lt;210&gt; 802

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g652 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 802

tttgtggaca	ttgcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
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ggttgtgtctg	agatttttgt	tttgactgtc	atggcttttg	atcgctatgc	tgctatctgc	180
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gcctgtgtctg	atacaactct	ggtaaatatg	ttggtgggtg	ccaacagtgg	tctcatctcc	420
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actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	cccca			635

&lt;210&gt; 803

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g653 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 803

ttgcctgaca	tcggtttcac	ctccacacgg	tccccaagat	gattgtggac	atccagtctc	60
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gaggcagggg	agagagacat	gtccttgagt	gtgatggcct	acgaccagtt	tgtagccatc	180
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tttccctgct	gccatatttg	gttttcttcc	catctcgggg	acccttttct	cttactctaa	480
aattgtttcc	tccattctga	gggtttcatc	gtcaggtggg	aggtataaag	ccctctccac	540
ctgtgggtct	cacgtgtcag	ttgtttgctg	agtttatgga	acaggcggtg	gagggtagct	600
cagttcggat	gtgtcatttt	ccccagaaa	gggtgcagtg	gcctcagtga	tgtacgcggt	660
tgtaaccccc						670

&lt;210&gt; 804

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g654 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

<400> 804  
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 atcaggaaag taatcagtta tctgtgctgt gtagccacagc ttttcatatt tctggccttg 120  
 ggggctactg aatatcttct cctggccgtc atgtcccttg ataggtttgt agctatttgt 180  
 cggcctctcc attactcagt tatcatgcac cagagactct gcctccagtt ggcagctgca 240  
 tccagggtta ctgggttttag taactcagtg tgggtgtcta ccctgactct ccagctgcca 300  
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 tcttgtgttg agacaacagc aaatgaggct gaactattcc ttgtcagtg gctcttccat 420  
 ctaatacccc tgacactcat ccttatatca tatgttttta ttgtccgagc agtattgagg 480  
 atacagctcg ctgaaggctg acaaaaagca tttgggacat gtgggttccca tctaattgtg 540  
 gtgtctcttt ttaatagtac agccgtctct gtgtacctgc aaccaccttc gccagctcc 600  
 aaggaccaag gaaagatggt ttctctcttc tatggaatca ttgcaccc 648

<210> 805

<211> 655

<212> DNA

<213> Unknown (H38g655 nucleotide)

<220>

<223> Synthetic construct

<400> 805  
 ttgcctgaca tccgtttcac ctccaccatt gtccccaaga tgattgtgga catccagtct 60  
 cacagcagag tgatctccta tgcaggccgc ctgactcaga tgtctctctt tgccattttt 120  
 ggaggcatgg aagacagaca tgcctctgag tgtgatggcc tatgaccggt tctagccat 180  
 ctgtcacccct ctatatcatt cagccatcat gaatccgtgt ttctgtggct tctactttt 240  
 gttgtctttt ttttttctca gtcttttaga cggccagctg cacaacttga ttgccttaca 300  
 aatgacctgc ttcaaggatg tggaaaattcc taatttcttc tgtgaccctt ctcaactccc 360  
 ccatcttgca tgttgtgaca ccttcaccaa taacataatc atgtattttc ctgctgccat 420  
 atttggtttt cttcccatct cggggaccct ttctcttacc gataaaattg tttcctccat 480  
 tctgagggtt tcatcatcag gtgggaagta taaagccttc tccacctatg ggtctcacct 540  
 gtcagatggt tctgattttt atggaacagg cgttggaggg tacctcagtt cagatgtgtc 600  
 atcttccccg agaaagactg cagtggcctc agtgatgtac acagtgggtca ccccc 655

<210> 806

<211> 662

<212> DNA

<213> Unknown (H38g656 nucleotide)

<220>

<223> Synthetic construct

<400> 806  
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 cacagcagag tcatctccta tgcaggctgc ccgactcaga tgtctctctt tgccattttt 120  
 ggagacacgg aagagagaca tgttctctgag tgtgggtggcc tatgaccggt ttgtagccat 180  
 ctgtcacccc ctatatcgtt cagccatctt aaaccctgtt ttctgtggct tctagattc 240  
 gttgtccttg gttttttttt ttttctcagt ctttttagact cccagctgca caacttgatt 300  
 gccttacaaa tgacctgctt caaggatgtg gaaattccta atttcttctg ggaaccttct 360  
 caactcccc atcttgcag ttgtgacatc ttcaccagga acatcaacct gtatttccct 420  
 gctgccatat ttgggtttct tccatctcg gggacgcttt tctcttgcta taaaattggt 480  
 tcttctattc tgagggtttc atcatcagg gtggaagtata aaccttctcc gcctgtgggt 540  
 ctcatctgtc agttgtttac tgattttatg gaacaggctt tggagggtac ctcagttcag 600  
 atgtgtcatc ttccccgaga aagactgcag tggcctcagt gatgtacgca gtggtcaccc 660  
 cc 662

<210> 807

<211> 647

<212> DNA

<213> Unknown (H38g657 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 807

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cacaagtcca	caatttccta	tgacgcctgc	ctctcccage	tcttcttctt	ccaccttctg	120
gctgggatgg	actgtttcct	gctgaccgcc	atggcctatg	accgactcct	ggccatctgc	180
cagccccca	cctacagcac	ccgcatgagt	cagacagtcc	agaggatggt	ggtggctgcg	240
tcttgggctt	gtgccttcac	caacgcactg	acccacactg	tggccatgtc	cacgctcaac	300
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tcctgtctta	gcacccaact	caatgagctg	ctgctctttg	tagcagcagc	cttcatggct	420
gtggcaccct	tgggtcttcat	cagtgtgccc	tatgcccctg	tggtagctgc	tgtgctgcaa	480
atcgctccgc	tgagggcaga	aagaaggcct	tctccacatg	tggctcccac	ctcactgtgg	540
tgggcatctt	ctatgggaca	ggtgtcttca	gctacatgag	gctgggttca	gtggaatctt	600
cagacaagga	taaggggggt	gggggttttca	tgactgtgat	caacccc		647

&lt;210&gt; 808

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g658 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 808

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gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgtcg	acatttttgt	tttgactgtc	atggcttttg	atcgctgtgc	tgctatctgc	180
caacccctcc	gttacactgt	catcatgagt	gctaattgct	atactgtgct	ggcatcactg	240
tcctgggttg	gggccttggg	tcattccttt	gttcagacct	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaccattac	ttttgtgatg	tccacccagt	cctaaaaactt	360
gcctgtgtcg	atacaactct	ggtaaatatg	ttgggtggtg	ccaacagtgg	tctcatctcc	420
ctgggggtgt	tcctcattct	tttggcctcc	tacacagtca	ttctgtttag	tcttcaaaaa	480
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aagctgtgtc	tgtgttctat	accaccatca	cccca			635

&lt;210&gt; 809

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g659 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 809

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ggagacctgg	agagcttctt	ccttgtggcc	atggcctatg	accgctatgt	ggccatctgc	180
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tcctgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttgtgt	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
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actctaaagg	acactgtcat	ggctatgatg	tacactgtgg	tgaccccc		648

&lt;210&gt; 810

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g660 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 810

actttgcaga	atatcacctc	cacttccatc	attttcctgc	tcactgggtg	tcctgggctg	60
gaagccttcc	acacctggat	ctccattccc	ttctgcttcc	tctctgtaac	tgctctcttg	120
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gatcgtttgg	tgccgtctct	atcccccttag	tatgccatga	tttaactgac	tcagatagct	420
aaaatgagtg	cagtgtat					438

&lt;210&gt; 811

&lt;211&gt; 1002

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g661 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 811

gcagggtgtg	aaaacgataa	tacaagttct	ttcgaaggct	tcactcctgg	gggcttctct	60
gatcgcccc	acctagagct	gatcgctctt	gtgggtgtcc	tcactcttta	tctgctgact	120
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&lt;210&gt; 812

&lt;211&gt; 827

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g662 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 812

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&lt;210&gt; 813

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g663 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 813

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&lt;210&gt; 814

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g664 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 814

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&lt;210&gt; 815

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g665 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 815

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&lt;210&gt; 816

&lt;211&gt; 649

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g666 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 816

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ccccagaaag	ggtgcagtg	cctcagtgat	gtacacgggtg	gtcaccccc		649

&lt;210&gt; 817

&lt;211&gt; 651

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g667 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 817

atcattgata	tttcgtatgc	ttccaacaaa	gtccccaaga	tgctgacaaa	ccttggtctg	60
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cctgaggagc	agcagaaggt	cctttccctg	ttttacagcc	ttttcaacc	g	651

&lt;210&gt; 818

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g668 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 818

ctagtggact	tttgttactc	ttcagctgtc	actcccacag	tcatagctgg	gctcggtata	60
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gccactgtgg	aaaatttctt	cttggcctca	atggcctatg	accgctatga	tgcagtgtgc	180

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ttctgccatc	ctagtaatcc	tggtctccta	cctattcata	tttatcacca	tcctagagat	480
gcactcagct	tcaggatacc	agaaggcttt	gtcceaactgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatcttcat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgttcta	tactatgatc	atcccc		646

&lt;210&gt; 819

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g669 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 819

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ccgggagtc	agatccccct	cttcttctctg	tttctaggct	tctacgtggt	cactgtggtg	120
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atgctgatga	gctttgtctt	aaagaagaac	agcatctcct	acgcagggtg	tatgactcag	300
ctcttctctc	ttcttttctt	tgtgtctctc	gagtccttca	tectgtcagc	aatggcgtat	360
gaccgctatg	tggccatctg	taacccactg	ttgtacatgg	tcaccatgtc	tccccagggtg	420
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gtgggtgcca	tgctcaaccc	attaatttat	agcctgagga	ataaggacgt	caaagttgct	900
ctaaagaaaa	tcttgaacaa	aatgcattc	tcc			933

&lt;210&gt; 820

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g670 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 820

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ggcaaaacc	tgaagagagt	gctcttc				927

<210> 821  
 <211> 887  
 <212> DNA  
 <213> Unknown (H38g671 nucleotide)

<220>  
 <223> Synthetic construct

<400> 821  
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 acaaaactccc gctgccccag tgttttattc ttaatgtggt ccctgtgggg agaatttgaa 120  
 cataatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180  
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240  
 atctcagaga ggaacatcat ctcttttgtg ggatggccaa cgtagctata tttcttttgc 300  
 atctttgtca aagaacctaa aaatgggggtc attgtgggaa taatgttctc agccaagatg 360  
 cttgtagccg agagataatg gactagtctg tgatgtgaaa ctagaaaatg cacatggccc 420  
 tagaaagggtc tgattttaga atgggataaa caggatctgc taaaaagaaa catttaatca 480  
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 acatattata atatgttttt atatttgaa acagaaaaaa ataagttatt tatatcacaa 660  
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 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840  
 actaccttct gaaaaagttg aaaacactgc tttataagaa cagctat 887

<210> 822  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g672 nucleotide)

<220>  
 <223> Synthetic construct

<400> 822  
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 ccagagttcc ggcaaccctt ctttttctct tttctagtgg tctacattgt caccatggta 120  
 ggcaaccctg gcttgatcat tcttttcggt cttaaattctc acctccacac accaatgtac 180  
 tatttctctt tcaatctctc ctccattgat ctctgttact cctctgtttt cactcccaaa 240  
 atgctaataga actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300  
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360  
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcagggtc 420  
 tgttctatgc tcacttttgc tgcttacata atgggattgg ctggagccac ggccccacacc 480  
 ggggtgcatt ttagactcac ctctgcagc gctaatatca tcaaccatta cttgtgtgac 540  
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 attgttgtgg gtattaatat catggtacct agttgtacca tcctcatttc ttatgttttc 660  
 attgtcacta gcattcttca tatcaaatcc actcaaggaa gatcaaaagc cttcagtact 720  
 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780  
 aaatattctt ctggatctat ggagcagggg aaagtttctt ctgttttcta cactaatgtg 840  
 gtgcccagtc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgcactg 900  
 aggaaagctc tgattaaaa tcagagaaga aatatattc 939

<210> 823  
 <211> 1071  
 <212> DNA  
 <213> Unknown (H38g673 nucleotide)

<220>  
 <223> Synthetic construct

<400> 823  
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ttttttctta gcaatctctc actcctggac ctttgcata ccacaagtac agttccacaa 240
atgctggtaa acatatgcaa caccaggaaa gtaatcagtt atgggtggctg tgtggcccag 300
cttttcattt tcctggcctt gggttccaca gaatgtcttc tcctggccgt catgtgcttt 360
gataggtttg tagctatttg tcggcctctc cattactcaa ttatcatgca ccagaggctc 420
tgcttccagt tggcagctgc atcctggatt agtggtctta gcaattcagt attacagtcc 480
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tgtggctccc atctaattgt ggtgtcactt ttttatggta cagctatctc catgtacctg 780
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tttgtcatta ctatagaaaa ctattgtaat ctccctcaaa gaaaatttcc t 1071

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&lt;210&gt; 824

&lt;211&gt; 991

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g674 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 824

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atggctcctg gaaatggctt tttcatgact aaaatcattt tgctggagtt aacagatcag 60
ccagatctcc aactccctct gttcttccctg tttctagtgt atgggtcactg cgttgggaaa 120
tttggtttgg taactctcgt tgtgtcctcaat tcacaccttc ataccccat gtactttttc 180
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ttttttcttt attttttttt ggtatttctg aatgctatgt gctcacctca atggcctatg 360
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catgtccccc aaagtgtact ctcaccttat gcttgggtta tacttgctag ctttttctag 480
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ctttctctga gaaaaaaacc ctagttagaa aaaattttga ctagaataag tatctttctg 960
tgcattgtatt tttaggacag ggagcttctg t 991

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&lt;210&gt; 825

&lt;211&gt; 997

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g675 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 825

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atggctcctg gaaatggctc tttgatgaat gaattcattc tgggtggggtt aacagactag 60
ccagatcttt aactccctct gttcttcatg tttcttgtaa tgtatgttgt cactgtgata 120
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ttacttccgt	gacatcctcc	ctgtgttcca	gctctcctgc	accagcacct	acatcaatga	600
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tctctgtgta	tgtagttaca	ggatggggat	tctctgt			997

&lt;210&gt; 826

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g676 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 826

atggacagtc	taaaccaaac	aagagtgact	gaatttgtct	tcttgggact	caactgataac	60
cgggtgctgg	aaatgctgtt	tttcatggca	ttctcagcca	tttatatgct	aacgctttca	120
gggaacattc	tcatacatat	tgccacagtc	tttactccaa	gtctccatac	ccccatgtat	180
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ctcaggcaga	gacaagtttt	tttcacgaaa	tcataataca			939

&lt;210&gt; 827

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g677 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 827

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acagatctcc	aaccgcccct	gttcttcctg	tttctagtaa	tggtgtgggt	tgctgggtag	120
gggaatttgg	gcttggtaac	tctgattgtg	ttcagttcac	actttcatgc	acccatgtac	180
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acattgatgt	agttcccatg	ataaactcct	caatttacag	cttaagaaac	aatgatgtta	900

aacttgccctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960  
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

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atgacagatg	cccttaaaaa	agtgtctggga	gtgccatcaa	aagaaatata	ttggaacaca	960
ctgaaa						966

<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

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ctgacactga	ttgggaatgt	tctcattgtc	ataactatta	tctatgacca	ccggctccat	180
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ctgcagtcac	ccccctgctg	aaccccatca	tctataccct	taggaatgaa	gaaatgaaga	900
gtgccttaaa	caagtttagtg	gggagaaaag	agagaaaaga	agaaaaatga	aaatgtctac	960
gtccttagga	tacgtgggtgc	tccaaattaa	agaagcgcct	tgc		1003

<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 830

acggggactg	gatgatggct	gtgtcatgcc	atgatcctaa	ctccccctcac	ttccagttac	60
cttactgtgg	cctaacaagg	tgggctatac	ttctgtgata	tccctgcagt	tacctctagc	120
ctgtaaggac	acatcccttag	cccagagggg	agggttttaca	aatgttggtc	ttttgtctct	180
catttgcttt	tttctcatcc	ttgtttccta	tacttgcatt	gggatttcca	tatcaaaaat	240
ccgctcagca	gagggcaggc	agcgggcctt	ctccacctgc	agcgtccacc	tcactgcaat	300
cctttgtgct	tatgggccag	tcatcgttat	ctatctacaa	cccaatccca	gtgccttgct	360
tggttccata	attcagatat	tgaataatct	ggtaacccca	atgttgaatc	cactaatcta	420
tagccttagg	aataaggatg	taaaatcaga	tcagccctga	ggaatgtatt	tcccaaga	478

&lt;210&gt; 831

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g681 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 831

ttactatttt	taatgttctt	tattacttcc	ttgggtcata	aattccatct	gatatcattt	60
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tgataacata	cactcacagc	attaatttat	tgtaaagtgt	ccttggtcta	gggtatagac	180
ctatttgtag	ggatataccct	ttagtccag	agtattgttc	ttatttctag	ggcgtgggtcc	240
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gcatttaaaa	ttctattgcc	ctagttgagg	gtaactgcta	aaatcttttc	tctcagccat	360
ctggctgctg	ttttctactt	actttcttag	agtcttgtct			400

&lt;210&gt; 832

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g682 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 832

atggctactt	caaaccattc	ttcaggggct	gagtttatcc	tggcaggcct	gacacaacgc	60
ccagaacttc	aactgccact	cttctctctg	ttccttgga	tatatgtggt	cacagtgggtg	120
gggaacctgg	gcatgatctt	cttaattgct	ctcagttctc	aactttaccc	tccagtgtat	180
tattttctca	gtcatttgct	tttcattgat	ctctgctact	cctctgtcat	tacccttaag	240
atgctgggtga	actttgttcc	agaggagaac	attatctcct	ttctggaatg	cattactcaa	300
ctttattttct	tccttatttt	tgtaattgca	gaaggctacc	ttctgacagc	catggaatat	360
gaccgttatg	ttgctatctg	tcgcccactg	ctttacaata	ttgtcatgtc	ccacagggtc	420
tgttccataa	tgatggctgt	ggtatactca	ctgggttttc	tgtgggccac	agtccatact	480
accgcactgt	cagtgttgct	attctgtagg	tctcatacgg	tcagtcatta	tttttgtgat	540
attctccctt	tattgactct	gtcttgctcc	agcaccacac	tcaatgagat	tctgctgttc	600
attattggag	gagttaatac	cttagcaact	acactggcgg	tccttatctc	ttatgctttc	660
attttctcta	gtatccttgg	tattcattcc	actgaggggc	aatccaaagc	ctttggcact	720
tgtagctccc	atctcttggc	tgtgggcac	tttttgggt	ctataacatt	catgtatttc	780
aagccccctt	ccagcactac	tatggaaaaa	gagaagggtg	cttctgtgtt	ctacatcaca	840
ataatcccca	tgctgaatcc	tctaattctat	agcctgagga	acaaggatgt	gaaaaatgca	900
ctgaagaaga	tgactagggg	aaggcagtc	tcc			933

&lt;210&gt; 833

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g683 nucleotide)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 833

atggtgatcc	tgtcctggga	aaaccaaacy	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tcctcctggg	gaacttgctc	tgtctggaga	tctgggtatac	ctctaaccac	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcaactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcacaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
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acataccttg	tgcctcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgtct	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggtg	tttgccctt		948

&lt;210&gt; 834

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g684 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 834

ccagtgagga	ccttggagac	tactaatatc	actggatttg	tgaatgagtt	catcctcttg	60
ggcttccctt	gccgctggga	gatccagatc	ctcctttttg	tgggtcttct	tctcatctac	120
cttctgaccc	tcctaggtaa	cacatccatc	atctgtgctg	tgtgggtcaag	ccagaaactc	180
cacacaccta	tgtacatcct	actggccaat	ttctccttcc	tgagagatctg	ctgtgtcagt	240
tctgacgtgc	ccataatggc	agccaatctc	atctcccaga	cacagagcat	ctcctgtgct	300
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gttctatact	ttgtcaactc	cattctttta	tcctctgata	tacagtcttc	ggaacaagga	900
tatgaaagag	gcactaaaga	aatttctgag	gaatcgccac	actgtc		946

&lt;210&gt; 835

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g685 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 835

cttatagcta	caggaaactg	gacaagaata	agtaagttaa	tcctcatgag	cttctcttcc	60
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cccaacatgc	tgtggaccct	gcttgcccag	gacacaacca	tctccttccct	tggtctgtgcc	300
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ctcacattgc	tgctgccatc	ctcaagatcc	catcagctaa	agggaagaat	aaagcctttt	720
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atgccctcag	caggacggtc	tctaaggccc	tagccctcag	aaactg		946

&lt;210&gt; 836

&lt;211&gt; 973

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g686 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 836

atggctgtgg	aaaatgactc	ttcagtgaca	agagtttatt	cttttgggat	taacagacca	60
gcctgagatc	taattgcccc	tgtttttccct	gttcttgggtg	aactatatga	ccaccatggg	120
gggcaacttg	agtttaatta	atctaatttg	cctgaattca	caccttcaca	ctcccatgta	180
ttttttccct	ttcaatctgt	ccttcattga	tctctgttat	tcatttgtct	ttaccccaa	240
aatgctgatg	agctttatct	cagagaggaa	catcatctcc	tttccaggat	gcgtaactca	300
gctcttttcc	ttctgctttt	ttgtccactc	tgagtgtcat	gtgctgacag	ccatggccta	360
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tctaaaggaa	accctaaata	aaattacaaa	ctgagtagag	ccaatgggtg	tgcccttagcc	960
cctctccaat	tgc					973

&lt;210&gt; 837

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g687 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 837

atgagataga	taaatacagac	acaagtgata	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggg	cactgtgctt	120
ggaaatctgc	ttctaattctc	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgct	tctggctgac	ctctatttct	ctaccaacat	acttctctag	240
gcactagtcc	acctgctttc	cataaacaac	ctcattgcat	tcacacttcc	tctaactcaa	300
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ccatgcttaa	tcccctcatc	tatagcctga	gaaacaagga	tgtgaaggca	gctctgagga	900
aagtagccac	aaggaatttc	ccatgaaggc	ttggaatctc	acactgacag	tgagctcaga	960
gaaccttttg	gcttcctact	tcaaagactt	gc			992

&lt;210&gt; 838

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g688 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 838

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgatttctat	cacgtgcacc	cagctcatte	accaacccat	gtatttcttc	180
ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgaaccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttgagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
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accatctctg	taccattttg	tggcccaaat	gatatagatc	actactctcg	cgatgtgtat	540
cctttgctg						549

&lt;210&gt; 839

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g689 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 839

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgagcgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	gtgatggcct	atgacctgtt	tgtagccatc	180
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tgtgggtctc	acctgtcagt	tgtttgctga	ttttatggag	caggcgttgg	aggggtacct	600
ggttcagatg	tgtcatcttt	cccagaaaag	ggtgcagtgg	cctcagtgc	gtacgtacac	660
ggtggtcacc						670

&lt;210&gt; 840

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g690 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 840

atggacgtca	ggctcatctg	caccaccgta	cccaagatgg	ccttcaacta	cttgtctggc	60
agcaagtcca	tttctatggc	tggctgtgcc	acacaaattt	tcttctgtgt	atcactgctt	120
ggctctgaat	gctttctgtt	ggctgttatg	tcttatgact	gctacattgc	catttgccac	180
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&lt;210&gt; 841

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g691 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 841

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ctccgagaag	caaggcatgt	cctttcccaa	gaaacttttc	cagaatcaca	aacttttctc	120
actctttgca	gggatgaatg	tatttctgca	gactgtgatg	gcctatgacc	actttgtggc	180
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tctggtgtcc	tggagcatga	gtgccctgaa	ttcctcactg	caaagcagaa	tgtgttgag	300
ctgtccttct	gcacaaactt	ggaaatcccc	ccattttttt	ctgtgaactt	aatcagttga	360
tctgcttgcc	ctgttctaac					380

&lt;210&gt; 842

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g692 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 842

tttgttgatt	tctgtttatc	caccacgatt	acacccaaac	tgctggagaa	cttgggttggt	60
gaagatagaa	ctatctcctt	cacaggatgc	atcatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aacctctctc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtggctacg	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
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acgccttcca	ctggggggcg	caagaaagcg	ttctccacgt	ctgcctccca	cttgacggcc	540
attaccattt	tccatgggac	tatccttttc	ctctactgtg	ttcctaactc	caaaagtctg	600
tggctcatgg	tcaagggtggc	ctctgtcctt	tacacagtgg	tcattccc		648

&lt;210&gt; 843

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g693 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 843

ttgccagaca	ttggttttcac	cttggccacg	gtccccaaga	tgattgtaga	catgcaatca	60
catagcagaa	tcattctccca	tgcaggctgt	ctgacacaga	tacctttctt	tgtccttttt	120
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cacctccctgc	actaccagct	catcatgaat	cctcacctct	gtgtcttctt	agtgttgatg	240
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tgttctgact	gtcatcagta	acatatccat	acgttttagat	agtactatat	ttggctttct	420
tcccatttca	gggatccctt	tgtcttacta	taaaattgtg	ccctccattc	taagaattcc	480
attgtcagat	gggaagtata	aagccttctc	cacctgcggc	tctcacctgg	caattgtttg	540
cttattttat	ggaacaggca	ttggcatgta	cctgacttca	gctgtgtcac	cagccccag	600
gaatgggtg	gtggcatcag	tgttgtacgc	tatggtcacc	ccc		643

&lt;210&gt; 844

&lt;211&gt; 652

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g694 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 844

ttgcctgaca	tcggtttcac	ccccaccacg	gtccccaaga	tgatttgtga	catccagtct	60
cacagcagag	tcattctatg	aggctgcctg	actgtgatgt	ctctctttgc	catttttgga	120
ggcatggaag	agacacatgc	tcctgaatgt	gatggcctat	gtccggtttg	tagccatctg	180
tcaccctcta	tatcattcag	ccatcatgaa	cccgtgtttc	tgtggcttct	tacttttggt	240
gtcttttttt	tttctcggtc	ttttagacgc	ccagctgcac	aacatgattg	ccttacaagt	300
gacctgcttc	aaggatgtgg	aaattcctaa	tttcttctgt	gaccttctc	aactcccca	360
tcttgcatgt	tgtgacacct	tcaccaataa	cataatcatg	tattttcctg	ctgccatatt	420
tggttttctt	cccatctcgg	ggacctttt	ctcttactat	gaaattgttt	cctccattct	480
gagggtttca	tcataagggtg	ggaagtataa	ggccttcgcc	acctgtgggt	ctcacctgtc	540
agtcgtttgc	tgattttatg	gaacaggcgt	tggagggtac	ctcagttcag	atgtgtcatc	600
ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	cc	652

&lt;210&gt; 845

&lt;211&gt; 692

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g695 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 845

ttgcctgaca	tcggtttcac	ctccaccaca	gtcgccaaga	tgatttgtga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgtccttgag	tgtgatggcc	tatgaccggt	ttgtagccat	180
ctgtcaccct	ctatatcggt	cagccatctt	gagcccggtg	ttctgtgcct	tcctagattt	240
gttgctcttg	ttttgttttg	ttttgttttg	ttttgttttg	ttttgttttg	ctcagtcctt	300
tagactccca	gctgcacaac	ttgattgcct	tacaaatgac	ctgcttcaaa	gatgtggaaa	360
ttcctaattt	cctctgggaa	ccttctcaac	tccccatct	tgcattgtgt	gacaccttca	420
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ccttttctct	tacaatggag	taaaattggt	tcctccactc	tgagggtttc	atcatcaggt	540
gggaagtata	aaccttctcc	acctgtgggt	ctcacctgtc	agttgtttgc	tgattttgtg	600
gaacaggcgt	tggagggtac	ctcggttcag	atgtgtcatc	ttccccgaga	aagagtgcag	660
tggcctcagt	gatgtacacg	gtggtcaccc	cc			692

&lt;210&gt; 846

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g696 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 846

atgctggcta	gaaacaactc	cttagtgact	gaatttatcc	ttgctggatt	aacagatcgt	60
ccagagttcc	ggcaaccctt	ctttttcctg	ttcctagtga	tctacattgt	caccatggta	120
ggcaaccctt	gcttgatcac	tcttttcggt	ctaaattctc	acctccacac	accaatgtac	180

tatttccctct	tcaatctctc	cttcattgat	ctctgttact	cctctgtttt	cactcccaaa	240
atgctaata	actttgtgtc	aaaaaagaat	attatctcca	atgttgggtg	catgactcgg	300
ctgtttttct	ttctcttttt	cgatcatctc	gaatgttaca	tgttgacctc	aatggcatat	360
gatcgctatg	tggccatctg	taatccattg	ctgtataaag	tcaccatgtc	ccatcaggtc	420
tgttctatgc	tcacttttgc	tgtttacata	atgggattgg	ctggagccac	ggccacacac	480
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gtgcccacgc	tcaatccccc	catctacagt	ttgaggaaca	aggatgtcaa	agttgcactg	900
aggaaagctc	tgattaaaaat	tcagaggaga	aatatatttc			939

&lt;210&gt; 847

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g697 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 847

atgaccatgg	aaaattattc	tatggcagct	cagtttgtct	tagatgggtt	aacacagcaa	60
gcagagctcc	agctgcccc	cttctcctg	ttcctgggaa	tctatgtggt	cacagtagtg	120
ggcaacctgg	gcatgattct	cctgattgca	gtcagccctc	tacttcacac	ccccatgtac	180
tatttccctca	gcagcttgtc	cttcgtcgat	ttctgtctat	cctctgtcat	tactcccaaa	240
atgctgggtga	acttccctagg	aaagaagaat	acaatccttt	actctgagtg	catgggtccag	300
ctctttttct	ttgtggtctt	tgtggtggct	gagggttacc	tcctgactgc	catggcatat	360
gatcgctatg	ttgccatctg	tagcccaactg	ctttataatg	cgatcatgtc	ctcatgggtc	420
tgtcactatgc	tagtgctggc	tgccttcttc	ttgggcttcc	tctctgcctt	gactcataca	480
agtgccatga	tgaaactgtc	cttttgcaaa	tcccacatta	tcaaccatta	cttctgtgat	540
gttcttcccc	tcctcaatct	ctcctgctcc	aacacacacc	tcaatgagct	tctacttttt	600
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atcctctaca	gcactcctca	catccgctcc	tcagagggcc	ggtccaaagc	ttttggaaca	720
tgcagctctc	atctcatggc	tgtggtgata	ttctttgggt	ccattacctt	catgtatttc	780
aagccccctt	caagtaactc	cctggaccag	gagaaggtgt	cctctgtatt	ctacaccacg	840
gtgatcccca	tgtgaacccc	tttaatatat	agtctgagga	ataaggatgt	gaagaaagca	900
ttaaggaagg	tcttagtagg	aaaa				924

&lt;210&gt; 848

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g698 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 848

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
ccagatctcc	agtccccctc	gttcttccctg	tttctagtaa	tctatgtggt	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttccctc	ttaacttgtc	cttcatagat	ctctgttatt	cttctgtgtt	tacacccaaa	240
atgctaata	actttatttc	agagaagaat	attatctcct	tcaaggggtg	catgacccaa	300
cttttctttt	tctgtttttt	ttgggtcattt	ctgaatgtta	tgtgctgacg	tcaatggcgt	360
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gtggttccca	tggtgaacct	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960
agtcacaaga	cagggatatt	ctgt				984

&lt;210&gt; 849

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g699 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 849

atgaaaccag	ggaatgagac	acaaatttca	caattccttc	tcctgggact	ttcagaggaa	60
ccagaattgc	agcccttcct	ctttgggcta	tttctgtcca	tgtacctggt	caccgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
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cacctccatg	ctgaacccct	tcattctacag	cctgagggaat	aaagacataa	acagagctct	900
gaatcgattc	ttcagagagc	agaaacagga	gggccatttt			940

&lt;210&gt; 850

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g700 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 850

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagtcggt	cctcgctttg	ctgtccctgt	ccctgtccct	gaatctggtc	120
acggtgtcga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccatgtact	tcttctctct	caacctgtgc	tgggctgaca	tcggtctcac	ctcggccacg	240
gttcccaagg	tgattctgga	tatgcagtcg	catagcagag	tcattctctca	tgtgggctgc	300
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caaagtgcc	tgcggagggt	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttcttgtg	t					971

&lt;210&gt; 851

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g701 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 851

cccattgagc	agggaaatta	caccaggggtg	aaggaatctc	ttttttcaag	gactgaccca	60
gtcccaagag	ctgagcttgg	tcttatttct	tttcttattt	tttgtgtact	cagcaactgt	120
gctgggtaac	ctcctcatca	tggctgtggg	gacctgtgag	tctcgcttc	acacccccac	180
gtacttctctg	ctctgcaatc	tctctgtgtt	ggttatctgc	ttctcctcca	tactgctcg	240
gaaggtgcta	atagaccttt	caagcagaaa	gaccatctcc	ttcaatgggt	gcatgacaca	300
gatgtttttc	ttccacctcc	tcgggtgggac	agacgttttt	tctctctttg	tgatggcggt	360
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gctgtctcca	tcacctttac	agtcattatt	cctgtcctga	accccatgat	ctacacctg	900
aggaaccagg	agatgaagtc	agccttgagg	aggcggaaga	aaagaccttc	tggaaaggga	960
tagatgctac	gaagtccaga	ttggaaaatc	agaactgaaa	agtatttctt	cata	1014

&lt;210&gt; 852

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g702 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 852

tctacatacc	cgcagaatth	aacagatgtc	tctttattcc	tcctcctaga	agctcagagg	60
atccagaaca	gcagcctgtc	ctcgctgggc	tgttcctgtc	catgtgcctg	gtcacgggtg	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acctcttctt	ctccaacctg	tccttgccctg	acatcggttt	cacctccagc	atggtcccca	240
agatgattgt	ggacatctaa	tctcacagca	gactcatctc	ctaggcaggc	tgctgactc	300
ccatgtctct	ctttgccatt	tttggaggca	tgggaagagag	acatgctcct	gagtgtgatc	360
cctatgaccc	gtttgtagcc	atctgtcacc	ctctatatca	ttcagccatc	atgaaccctg	420
gtttctgtgg	ctttctagtt	ttgttgtctt	ttttttctca	gtctctttta	gacgccagg	480
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aaagcgtcct	gcggcgggcg	cacggcagca	cagtctaagt	tcaatatctc	cttatctgtt	960
ccatgccttt	tgtagtgtgg	gttaaaaaag	gcagcaagggt	caaa		1004

&lt;210&gt; 853

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g703 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 853



atgaaaaact	gtaccaggg	aaaagaattt	attttccttg	gcctaacc	gaatggggac	60
acaagattgg	tcctatttct	tttcttactc	ttgggtgtaca	tgacgactct	gctgggaaac	120
ctcctcatca	tggtcactgt	cacctgtgaa	tcttgccctc	acatgcccat	gtattttttg	180
ctccataatt	tatctattgc	cgatatctgc	ttctactcca	tcacagagcc	caagggttctg	240
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aacccttgat	ctacactctg	agaaaccatg	agatgaagtc	aaccatgaag	agactgaaga	900
ctctgacctt	ctgataggaa	atagaccagt	gcttccctcc	ttctc		945

&lt;210&gt; 854

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g704 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 854

cacacagagc	cacggaatct	cacaggtgtc	tgaaaagtgc	tcctggggact	ctctctgaga	60
ggatccagaa	ctgcagccca	tcctcgctgg	gctgtccctg	tccatgtatc	tggtcacggg	120
gctgaggaac	gtgctcatca	tcctggctgt	cagctctgac	tcccacctcc	acacccccat	180
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acagatatct	ttcttgggtc	tttttgcatg	tatggaagac	atgctcctgt	gatggcctat	360
gacagagttg	tggtccatctg	tcacccctcg	cactatccag	tcacatgaa	tcctcacctt	420
cgtgtcttct	tagttttgtc	gtcctttttc	cttagcttgt	tggtattcca	gctgcacagt	480
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ctgcggaggc	tgctgcagcag	aacagtcgaa	tctcatgatc	tgttccatcc	tttttcttgt	960
gt						962

&lt;210&gt; 855

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g705 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 855

aagcagcagg	aaaatgggac	ctgtctgggtg	acagaattcc	tgatgatggg	attctccaac	60
ctccacacac	tgaggaacac	actcttcacc	ctgttcttcc	ttacctacct	ggtcacctc	120
ggtggcaacg	tcaccatcat	caccatcacc	catgcggata	gggtcccgcca	cactcccatg	180
taccacttcc	tggtgggtgt	gtccctctcg	gagacctgct	atacacgctg	gtcaccatcc	240
ccagcatgtc	ggctcatctg	ctgatggaga	ccaggccatc	tccatccctg	gctgtcaggc	300
tcagatgttt	ttcttctctg	gtctgggatg	cagccactgc	ttcctcctta	ccctgatggg	360
ttatgaccgc	tatgtggcca	tctgccaccc	cctgcgctac	tctatgggtca	tgagaccac	420
cgtttgcctc	tgctggggag	ccctgggtttt	ctgctctggg	ttctcggtgg	ccttgatcga	480

```

gaccagcatg atcttctcat cgcccttttg cggcggagac cacgtggagc acttcttctg 540
tgacatcgcc ccggtgctga agctcagctg cgccaagagt gccagcaagg cgctgggcat 600
ctttttcctg agcgtcctgg tgggtgctgat gtcttcgtc ccgacccctt tctcctatgc 660
cttcatcgctg gctgccatcg tgaggatttc cttggcagcc ggccggcgca aggccttctc 720
cacctgtgtg gcccacgtca ccgtggctcg agtacatttt gactgcgcct ccatcatcta 780
cttgcgctccg gagtccgggg ccaaccccca ccaggaccgc ttggtggctg tgttctacac 840
ggtggtgatg ccactgctga accctgtggt gtgcactctg tggaacaagg aggtgagagt 900
ggctctgagg aggaccctgg cgtggagccg tggggttttt aaataagaat ct 952

```

&lt;210&gt; 856

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g706 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(339)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 856

```

ctgctggacc acttcatctg tgagctgccg gcgttgctca agctggcctg cggaggcgac 60
ggagacacta ccgagaacca gatgttcgcc gcccgcgctg tcatcctgct gctgccgttt 120
gccgtcatcc tggcctccta cggtgccgtg gcccgagctg tctgttgcat gcggttcagc 180
ggaggccgga gggaggggcg tgggcacgtg ttgggtccca cctgacagcc gtctgctgt 240
tctacggctc ggccatctac acctacctgc agcccgcgca gcgctacaac cagcacgggn 300
ncagnttcgt atcgtctctt tacacctgtg gtcacaccc 339

```

&lt;210&gt; 857

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g707 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 857

```

atggatcaga gaaattacac cagagtga aaatttacct tctgggaat tactcagtc 60
cgagaactga gccaggctct atttaccttc ctgttttttg tgtacatgac aactctaattg 120
ggaaacttcc tcatcatggt tacagttacc tgtgaatctc accttcatac gcccatgtac 180
ttcctgctcc gcaacctgtc tattcttgac atctgctttt cctccatcac agctcctaag 240
gtcctgatag atcttctatc agagacaaaa accatctcct tcagtggctg tgctactcaa 300
atgttcttct tccaccttct gggggggagca gacgtttttt ctctctctgt gatggcggtt 360
gaccgctata tagccatctc caagccccct cactatatga ccatcatgag tagggggcga 420
tgcacaggcc tcatcgtggg ctctctgggt ggggggcttg tccactccat agcgagatt 480
tctctattgc tccactccc tgtctgtgga cccaatgttc ttgacacttt ctactcgat 540
gtcccccagg tctcaaaact tgctgcact gacaccttca ctctggagct cctgatgatt 600
tcaaataatg ggttagtcag ttggtttgta ttcttcttct tctcatactc ttacacggtc 660
atcttgatga tgctgaggtc tcacactggg gaaggcagga ggaaagccat ctccacctgc 720
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cccttcaact ccctcccac agacactgcc atctctgtca ccttcaactgt catctccct 840
ttgctcaatc ctataattta cagctgagg aatcaggaaa tgaagtggc catgaggaaa 900
ctgaagagac ggctaggaca atcagaaagg attttaatt 939

```

&lt;210&gt; 858

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g708 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 858

gtagccatat	gtaatccctt	gctttatcca	gtgatgatgt	ccaacaaact	cagcgctcag	60
ttgctaagta	tttcatatgt	aattggtttc	ctgcaccttc	tggttcatgt	gagtttacta	120
ttgcgactaa	ctttctgcag	gtttaacata	atacattatt	tctactgtga	aattttacaa	180
ctgtttcaaaa	tttcatgcaa	tgggccatct	attaacgcac	taataatatt	tatttttggt	240
gctttttatac	aaatacccac	tttaatgact	atcataatct	cttataactcg	tgtgctcttt	300
gatattctga	aaaaaaagtc	tgaaaagggc	agaagcaaag	ccttctccac	atgcggcgcc	360
catctgcttt	ctgtctcatt	gtactacgga	actctgatct	tcattgtatgt	gcgtcctgca	420
tctggcttag	ctgaagacca	agacaaagtg	tattctctgt	tttacacgat	tataattccc	480
ctgcta						486

&lt;210&gt; 859

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g709 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 859

atgtactact	tcctctgcca	cctggccttg	gtagacgcgg	gcttcactac	tagcgtggtg	60
ccgccgctgc	tggccaacct	gcgcggacca	gcgctctggc	tgccgcgcag	ccactgcacg	120
gccagctgtg	gcgcacgcgt	ggctctgggt	tcggccgaat	gcgtcctcct	ggcgggtgatg	180
gctctggacc	gcgcggccgc	agtgtgccgc	ccgctgcgct	atgcggggct	cgtctccccg	240
cgcctatgtc	gcacgctggc	cagcgcctcc	tggctaagcg	gcctcaccaa	ctcgggttgcg	300
caaaccgcgc	tcctggctga	gcggccgctg	tgcgcgcccc	gcctgctgga	ccacttcatc	360
tgtgagctgc	cggcggttgc	caagctggcc	tgcggaggcg	acggagacac	taccgagaac	420
cagatgttcg	ccgcccgcgt	ggtcatectg	ctgctgccgt	ttgccgtcat	cctggcctcc	480
tacggtgccg	tggcccagac	tgtctgttgc	atgcggttca	gcggaggccg	gaggagggcg	540
gtgggcacgt	gtgggtccca	cctgacagcc	gtctgcctgt	tctacggctc	ggccatctac	600
acctacctgc	agcccgcgca	gcgctacaac	caggcacggg	gcaagtctgt	atcgctcttc	660
tacaccgtgg	tcacacctgc	tctcaaccgc	ctcatctaca	ccctcaggaa	taagaaagtg	720
aagggggcag	cgaggaggct	gctgcggagt	ctggggagag	gccaggctgg	gcag	774

&lt;210&gt; 860

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g710 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 860

atgcagagag	ccaatcactc	cacagtgacc	caattcatcc	tcgtcggctt	ctctgtcttc	60
ccccacctcc	agctgatgct	cttctgtctg	ttctgtctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcacatggc	caccgtctgg	agcgagcgca	gcctccacac	gccatgtac	180
ctcttctgt	gcgcctctc	cgtctccgag	atcctctaca	ccgtggccat	catcccgcgc	240
atgctggccg	acctgctgtc	caccagcgc	tccatcgctt	tcttgccctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggttcacc	cactccttcc	tgctcaccgt	catgggctac	360
gaccgctacg	tggccatctg	ccaccccctg	cgtacaacg	tgctcatgag	cccgcggggc	420
tgcgcctgcc	tgggtggctg	ctcctgggct	gggtggcttg	tcattggggat	ggtggtgacc	480
tcggccattt	tccacctcgc	cttctgtgga	cacaaggaga	tccaccattt	tgcttgccat	540
gtgccacctc	tgttgaagtt	ggcctgtgga	gacgatgtgc	tgggtggtgg	caaaggcgtg	600
ggcttggtgt	gtatcacggc	cctgctgggc	tgttttctcc	tcctcctcct	ctcctatgcc	660
ttcatcgtgg	ccgccatctt	gaagatccct	tctgctgaag	gtcggaaaca	ggccttctcc	720
acctgtgcct	ctcacctcac	tgtggtgggc	gtgcactatg	gctttgcctc	cgctatttac	780
ctgaagccca	aaagtcccca	gtctctggaa	ggagacacct	tgatgggcat	cacctacacg	840
gtcctcacac	ccttctctcag	ccccatcatc	ttcagctcca	ggaacaagga	gctgaaggctc	900
gccatgaaga	agaccttctt	cagtaaactc	taccagaaaa	aaaatgta		948

<210> 861  
 <211> 674  
 <212> DNA  
 <213> Unknown (H38g711 nucleotide)

<220>  
 <223> Synthetic construct

<400> 861  
 ttgcctgaca tcgggtttcac ctccaccacg gtccccaaga tgattgtgga catccagtct 60  
 cacagcagag tcctctccta tgcggggtgc ctgatcagat gtctctcttt gccacttttg 120  
 gaagcatgga agagaggcat gctcctgagt gtgatggcat atgaccgggt tgtagccatc 180  
 tgtcacccctc tatatcggtc agccatcttg aaccctgat tctgtggctt cctagatttg 240  
 ttgtctttgt ttttttttgt ttgtttgttt tgtttttctc agtcttctag actcccagct 300  
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360  
 ctgggaacct tctcarctcc cccatcttgc atgtttgtgac accttcacca ggaacatcaa 420  
 catgtatttc cctgctgccg tatttggttt tcttcccatc tcagggacct tttctcttac 480  
 tgtaaaattc tttcctccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540  
 ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaacaggc gttggagggt 600  
 acctcgggtc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660  
 ygggtggctac cccc 674

<210> 862  
 <211> 653  
 <212> DNA  
 <213> Unknown (H38g712 nucleotide)

<220>  
 <223> Synthetic construct

<400> 862  
 ttgcctgaca tcgggtttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60  
 acagcagagt catctcctat gcaggccgcc tgactcagat gtctctcttt gccatttttg 120  
 gaggcattgga agagagacat gctcctgagt gtgatggcct atgaccgggt tgtagccatc 180  
 tgtcacccctc tatgtcatte agccatcacg aaccctgtgt tctgtggctt tctagttttg 240  
 ttgtcttttt tttttctcag tcttttagac gccagctgc acaacttgat tgccttacaa 300  
 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360  
 gtcttgcatg ttgtggcacc ttcaccaata acataatcat gtatttccct gctgccatat 420  
 ttggttttct tcccatctcg gggaccttt tctcttacga taaaattgtt tcttccattc 480  
 tgagggtttc atcatcaggt gggaagcata aggcttctc caccaggggg tctcacctgt 540  
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcggttca gatgtgtcat 600  
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863  
 <211> 648  
 <212> DNA  
 <213> Unknown (H38g713 nucleotide)

<220>  
 <223> Synthetic construct

<400> 863  
 ctggtggact ttggatactc ctacagctgc actcccaagg tcatggctgg gttccttata 60  
 gaagacaagg tcattctctta caatgcatgt gctgtctaaa tgtatatctt tgtagctttt 120  
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180  
 aaaccctac attacaccac aaccatgaca acaactgtgt gtgctcgtct ggccataggc 240  
 tctacacctt gtgggtttct gaatgcctcc atccacactg gggacacatt tagtctctct 300  
 ttctgtaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catggttctc 360  
 tcttgctctg atagacatat tagcgagctt gttcttattt atgttgtgag cttcaatatc 420  
 tttatagctc tctggttat cttgatatcc tacacattca tttttatcac catcctaaag 480

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atgcactcag cttcagtata ccagaagcct ttgtccacct gtgcctctca tttcattgca      540
gtcggcatct tctatgggac tattatcttc atgtacttac aaccagctc cagtcactcc      600
atggacacag acaaaatggc acctgtgttc tatacaatgg tcatcccc      648

```

&lt;210&gt; 864

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g714 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 864

```

attgttgaca tatcctatgc ttccaactat gtccccaaga tgctgacgaa tcttatgaac      60
caggaaagca ccatctcctt ttttccatgc ataatgcaga cattcttgta tttggctttt      120
gctcacgtag agtgtctgat tttggtggtg atgtccctatg atcgctatgc ggacatctgc      180
caccctttac gttacaatat cctcatgagc tggagagtgt gcactgtcct ggctgtggct      240
tcctgggtgt tcagcttcct cctggctctg gtccctttag ttctcctcct gaggctgccc      300
ttctgcgggc ctcatgaaat caaccacttc tgtgaaatcc tgtctgtcct caagttggcc      360
tgtgttgaca cctgggtcaa ccagggtggtc atctttgcag cctgctgtgt catcctgggtg      420
gggccaactct gcctgggtgt ggtctcctac ttgcgcaccc tggcgcgcat cttgaggatc      480
cagtctgggg agggccgcag aaaggccttc tccacctgct cctcccaact ttgcgtgggtg      540
ggactcttct ttggcagcgc cattgtcacg tacatggccc ccaagtcccg ccacccctgag      600
gagcagcaga aagttctttc cctgttttac agccttttca atcca      645

```

&lt;210&gt; 865

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g715 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 865

```

gtggccatct gtaaaccctt tcattatgtg gtcacatga acaacagggt gtgtacctta      60
ttagttctct gctgttggtt ggctggcttg atgatcattg ttccaccact tagcttaggc      120
ctccagctcg aattctgtga ctccaatgcc attgatcatt ttagctgtga tgcaggctct      180
ctcctaaaga tctcatgctc agatacatgg gtaatagaac agatgggttat acttatggct      240
gtatttgcac tcattatcac cccagtttgt gtgattctgt cctacttgta catagtcaga      300
acaattctga agttcccttc tgttcagcaa aggaaaaagg ctttttctac ctgttcatcc      360
cacatgattg tggtttccat tgcctatgga agctgcatct tcatttatat caagccctct      420
gcaaaagatg aggtggccat aaataaagga gtttcagttc ttactacttc tgtcgcaccc      480
ttgttg      486

```

&lt;210&gt; 866

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g716 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(670)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 866

```

ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga catccagtct      60
cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccattttt      120
ggaggcatgg aagagagaca tgctcctgag cgtgatggcc tacgaccagt ttgtagccat      180
ctgtcacccct ccatatcggt cagccatctt gaaccctgtt ttctgtggct tccaagattt      240

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gttgctccttg	tntttttttt	tttttttttt	tttttctca	ggctttttaga	ctcccagctg	300
cataacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaatttc	taatgtcttc	360
tgggaacctt	ctcaactctc	ccatcttgca	tgttggtgaca	ccttcaccag	gaacatcagt	420
atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gacctttttc	tcttactgta	480
aaattgtttc	ctccattctg	agggtttcat	catcaggtgg	gaagtataaa	ccttctccac	540
ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggtgttg	gagggtacct	600
cagttcagat	gtgtcatctt	ccctgagaaa	ggctgcagtg	gcctcagtga	tgtacaagat	660
ggtcaccccc						670

&lt;210&gt; 867

&lt;211&gt; 654

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g717 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 867

ttggctgaca	tcggtttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcctctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctgttttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggg	ttgtagccat	180
ctgtcaccct	ctatattatt	cagccatcat	gaaccatgt	ttctgtggct	tcctagtttt	240
gtgttttttt	tttttctcag	tcttttagac	tcccagctgc	acaatttgat	tgccctacaa	300
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catcttgcat	gttggtgacac	cttcaccatt	aacatagtca	tgtatttccc	tgccgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttcctccatt	480
ctgagggttt	catcatcagg	tgggaagtat	aaagccttct	ccacctgtgg	gtctcacctg	540
tcagttgttt	gctgagttta	tggaaacaggc	gttgagggtt	acctcagttc	agatgtgtca	600
tcttccttga	gaaaggctgc	agtggcctca	gtgatgtaca	cgggtggtcac	cccc	654

&lt;210&gt; 868

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g718 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 868

ttgattttct	tcttaatcta	tccgcttctc	ctgggtgggt	atgaccagat	cctgggtggt	60
gtgatggcag	aggccagcct	tcacaagcct	gtgtacttct	tcctgataaa	cctctcagcc	120
ctagacatcc	tctccactac	agtcactgtc	cccaagacgc	tgccctgtt	cttgcttggg	180
gaccacttcc	tcagcttccc	tgctgtcttc	ctacagatgt	acctgttcca	cagcttctcc	240
tgctcagaag	ccttcatect	gggtgtcatg	gcctatgacc	gctatgtagc	tatctgccac	300
ccactgcaat	accctgttct	catgaaccca	cagaccaatg	ctgtcttggc	aaccgggtgcc	360
tggctcactg	ccctcctcct	gccatttcca	gcagtagtac	agacctccca	gatggcattt	420
gacagcattg	ctgacatcta	ccactgcttc	tgtgatcatc	tggctgtggg	ccaggcctcc	480
tgctctgata	ccacccccag	accttcattg	gtttctgcat	cgccatgggtg	gtgtccttcc	540
tcccccttct	cctgggtgctt	ctctcctatg	cccacatctt	gacctcggtg	cttcgcatta	600
actcccaaga	aggacgctcc	aaagccttct	ccacctgcag	ctcccatctc	ccggtagtgg	660
gcacctacta	ctcatccatt	gccatagcct	atgtggccta	cagcgtgac	ctgcccctcg	720
acttccacgt	catgggcaat	gttgtagatg	tcttcttctt	cctcttcttc	ttcttcttcc	780
tcttctctct	cttctctctc	ctcttcgtct	tcttcttctt	cttcttcttc	ttcttcttcc	840
tcttctctct	cttctctctc	tcttcttctt	tcttcttctt	tt		882

&lt;210&gt; 869

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g719 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 869

atggagatgg	aaaactgcac	cagggtaaaa	gaatttattt	tccttggcct	gaccagaat	60
cggaagtga	gcttagtctt	atctcttttc	ctactcttgg	tgtatgtgac	aactttgctg	120
ggaaacctcc	tcatcatggt	cactgttacc	tgtgaatctc	gccttcacac	gcccattgat	180
tttttgctcc	ataatttatc	tattgccgat	atctgcttct	cttccatcac	agtgcccaag	240
gttctgggtg	accttctgtc	tgaaagaaag	accatctcct	tcaatcattg	cttcactcag	300
atgtttctat	tccaccttat	tggaggggtg	gatgtatttt	ctctttcggt	gatggcattg	360
gacgatgatg	tggccatctc	caagcccctg	cactatgcga	ctatcatgag	tagagaccaa	420
tgcattgggc	tcacagtggc	tgccctgggtg	gggggctttg	tccactccat	cgtgcagatt	480
tcctgttgct	tccactccc	tttctgcgga	cccaatgttc	ttgacacttt	ctactgtgat	540
gtccaccggg	tcctcaaact	ggcccataca	gacattttca	tacttgaact	actaatgatt	600
tccaacaatg	gactgtctac	cacactgtgg	tttttcctgc	tcctgggtgtc	ctacatagtc	660
atattatcat	tacccaagtc	tcaggcagga	gagggcagga	ggaaagccat	ctccacctgc	720
acctcccaca	tcactgtggt	gacctgcat	ttctgtgccc	tgcattctatg	tctatgcccg	780
gcccttcaat	gccctcccca	tggataaggc	catctctgtc	accttcaatg	tcattctccc	840
tctgtccaac	cccttgatct	acactctgag	gaacctagag	atgaagtcag	ccatgaggag	900
actgaagaga	agacttgtgc	cttctgatag	aaaa			934

## &lt;210&gt; 870

## &lt;211&gt; 898

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g720 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 870

acaatgcagc	aaaataacag	tgtgcctgaa	ttcatactgt	taggattaac	acaggatccc	60
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cagcccttgt	tgaaacttgc	ctgcatggac	acttacatga	tcaacctgct	gttgggtgtc	600
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tctcacataa	ttgtagtcat	cttattcttt	ggcccatgta	tattcatata	tacacgcccc	780
ccgaaccatt	tccccatgga	caagatgggt	gcagtatttt	atactatttg	aacacccttt	840
ctcaatccac	tcattctacac	atctgaggaa	tgcagaagtg	aaaaatgcc	tgagaaa	898

## &lt;210&gt; 871

## &lt;211&gt; 943

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g721 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 871

atggagtgtg	gaaatgtcac	cagagtaaaa	gaatttatat	ttctgggact	tactcaatcc	60
caagaccaga	gtttggtctt	gtttcttttt	ttatgtcttg	tgtacatgac	gactctgctg	120
ggaaacctcc	tcatcatggt	caccgtgacc	tgtgagcttc	gccttcacac	ccccattgat	180
ttcctgctcc	gcaatctagc	catccttgac	atctgcttct	cttccacaac	tgctcctaaa	240
gtcttgtctg	accttctgtc	aaagaaaaag	accatatact	atacaagctg	catgacacag	300
atattctctc	tccactcct	tggtggggca	gacatttttt	ctctctctgt	gatggcggtt	360
gactgctaca	tggccatctc	caagcccctg	cactatgtga	ccatcatgag	tagagggcaa	420

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gtcccccagg	tcctcaaact	cacttgcact	gacacttttg	ctcttgagtt	cttgatgatt	600
tccaacaatg	gcctggtcac	taccctgtgg	tttatcttcc	tgcttgtgtc	ctacacagtc	660
atcctaata	cgctgaggtc	tcaggcagga	gggggcagga	ggaaagccat	ctccacttgc	720
acctccccac	atcactgtgg	tgaccctgca	ttttgtgccc	tgcatctatg	tctatgcccc	780
gcccttctact	gccctcccca	cagaaaaggc	catctctgtc	accttctactg	tcactctcccc	840
tctgctgaac	cctttgatct	acactctgag	gaaccaggaa	atgaagtcag	ccatgagaag	900
actgaagaga	agactcgtgc	cttctgaaag	ggaatagaaa	aca		943

&lt;210&gt; 872

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g722 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 872

atgctggggc	taaaccacac	ctccatgtct	gaattcatcc	tcgtcggett	ctctgccttc	60
ccccacctcc	aactgatgt	cttccctgtg	ttccctgtga	tgtacctgtt	cacgtgtgtg	120
ggcaacctgc	tcactatggc	caccgtctgg	agcgagcgca	gcctccacac	gccccatgtac	180
ctcttccctgt	gcgtccctctc	agtctccgag	atccctctaca	ccgtggccat	catcccgccg	240
atgctggccg	acctgctgtc	caccacagcg	tccatcgcc	tcctggcctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggttccacc	cactccttcc	tgctcaccgt	catgggctac	360
gaccgctacg	tggccatctg	ccacccccctg	cgctacaacg	tgctcatgag	cccacggggc	420
tgcgccctgcc	tgggtgggctg	ctcctgggct	gggtggctcg	tcattggggat	gggtgggtgacc	480
tcggccattt	tccaactgac	tttctgtgga	tcccatgaga	tcacagcattt	tttatgtcat	540
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ttcatcggtg	ccgacatctt	gaagatccct	tctgctgaag	gtcggaacaa	ggccttctcc	720
acctgtgcct	ctcaccttat	tgtgggtcatt	gtgcaactatg	gctttgcctc	tgctcatctac	780
ctcaagccca	aagggtcccca	ctctcaggag	gggtgacacc	tgatggccac	cacctacgca	840
gtcctcaagc	ccttccctcag	ccccatcatc	ttcagcctca	ggaacaaaaga	actgaaggtt	900
gccatgaaga	ggaccttctc	cagcacactc	tattcctcag	gc		942

&lt;210&gt; 873

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g723 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 873

atgcctgggtc	agaactacag	aaccatatct	gaatttatcc	tctctgggett	ctcagccttc	60
ccccagcagc	tcctgcctgt	cttggttccctg	ctgtacctcc	tgatgttcc	gttcacattg	120
cttggcaacc	ttcttatcat	ggccacagtt	tggattgaac	gcagactcca	cacacccatg	180
tacctcttct	tgtgtgccc	ctccatctct	gagattctgt	tcactgttgc	catcacccct	240
cgcattgttg	ctgatctgct	cttcacccat	cgttccatca	cctttgtggc	ttgtgccatt	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcat	ggtcattgggc	360
tatgatcact	acgtgaccat	ctgccaccca	ctgcattaca	acatgcta	gagtcaccgt	420
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tacctcaaac	ccaagggcct	ccattctatg	tacagtgtg	ccttgatggc	caccacctat	840
actgtcttca	cccccttct	cagcccaatc	attttccagtc	taaggaacaa	ggagctgaag	900
aatgccataa	ataaaaactt	ttgcagaagg	ttctgccctc	taagctcc		948



<210> 874  
 <211> 484  
 <212> DNA  
 <213> Unknown (H38g724 nucleotide)

<220>  
 <223> Synthetic construct

<400> 874  
 ggatggaaat acaagcacct tcaacatctc ctgcaccaag ttcttctctg tgggtttccc 60  
 tggacttcga gagtgggtggc cccttctggg cctgcctctt gtcttctctt ttgtgaccat 120  
 catctctgcc aatgccctgg tcatccacac agtgggtgcc cggcaaaatc tgcatacagc 180  
 tacgtgtatg ctcatcactg tgctcctggc tgtcaatatt cgtgctgcca cagccgtgat 240  
 gcctaaaatg ctggagggtt ttgtatatta tgctaaccac atatcgctgc atggccgcct 300  
 ggcctagggt ttcttttatct acttcaccct cctcctggac tacaacttcc tctggccctg 360  
 gccctggact ggttactttg ccactctgcca cccactctgc ttttctgacc tgatgacctc 420  
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgacccgcg 480  
 ccct 484

<210> 875  
 <211> 595  
 <212> DNA  
 <213> Unknown (H38g725 nucleotide)

<220>  
 <223> Synthetic construct

<400> 875  
 gtagccatct ggccaccctc tctgttttca aactgaatga ctccccagct ggctgggatt 60  
 gctggccatt cttgccttga cacagagctg gggagtgcga gtgcctttgg tagtactaac 120  
 tgcaaaagcc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcattgc 180  
 actgctgagc atagcttgtg gagacctgac cttcaacaac tggctggggc tggctatgtg 240  
 tttggctact gtaatctctg atatggccct gctggggacc tcctacaccc acatcatcta 300  
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360  
 ccacctactg gtcactctct ccactctacgt ctctggtctt tccacttcca tcaccttctg 420  
 agtagccaag actgtgtccc agaattgtcca gaatctactc agtgccatat acttgctgct 480  
 tccaggagcc ttgaatcctg tcattttatgg ggtgaggact agggagatcc agcaacatgt 540  
 agaaaagatg ctctgtgaaa aggaaacagc ccagaaggct ggggagaagc caaag 595

<210> 876  
 <211> 944  
 <212> DNA  
 <213> Unknown (H38g726 nucleotide)

<220>  
 <223> Synthetic construct

<400> 876  
 ttcagtcaga acttgctgat ctctgggtct gggctcctttg tcctgctggg gatgccggga 60  
 ctggaggctc tgcatacctg gctctctgtg cctgtgtgcc tgctctacat ggcagctttg 120  
 gtagggaatg cccttctagt ggggctgggt ggtcgctgac aaggcactct gggcaccat 180  
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240  
 caaagctctg gctgtacttt ggggcttgct tagtgagata tcattttggag gctgcttggtc 300  
 tcaactcttt gttgcccatg tgtcaatcat tgccacattg ctgagctctc agtgctgctg 360  
 tccacggccg tagactgcca gcctttgcgc tatggggcgt tgctggccca gtttgtggta 420  
 ggtctagtgg ctctgactac catgaccctg gatgtctgtg tcatgtacac cctgtgatcc 480  
 tgttcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgccaacaca 540  
 tgggtgtggc ttgcctggca tgtggagata cgtgccccat catcaggatg ggactggcca 600  
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcttat gccctcattt 660  
 tccgtgctgt ctgccgtctg ccactcccat ttgcctgcca caaggctctg ggtaactgctg 720

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aggctcagga	acttgcttca	acttttctgg	gcaggagcag	tga		944

&lt;210&gt; 877

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g727 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 877

atgaattggg	aaaatgagag	ctccccaaaa	gagtttatac	tacttggctt	ctcagatagg	60
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ggcaatgtgt	ccatcatgat	ggtgtgcatt	ctggatccca	aacttcatac	tcccatgtat	180
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caaccacctt	catccacctc	taaggactgg	ggaaagatgg	ttccctctt	ctatggaatc	840
atcacatcca	tgttgaactc	cctcatctac	agccttagaa	ataaagatat	gaaggaggcc	900
ttcaagaggc	tgatgccaag	aatctttttc	tgtaaagaaa			939

&lt;210&gt; 878

&lt;211&gt; 968

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g728 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 878

ggcacattga	atttaagtag	cttcaatcca	ggactcttca	ttctgttggg	gatcccaggg	60
ctggagtgg	tctgcatctg	gatgggaatt	ctctccttta	ccagttacct	tgtctccctt	120
gcagggaatg	tcaccttct	ctaccttate	actgtggaac	acaacctcca	taaaccctatg	180
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aaaacatttg	ggatattcta	gctgaaagct	cagaaaaataa	tatttctctg	atgcttcacc	300
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agattggaaa	caaggtcata	cttttattct	ttcttaaagg	gatgcagtga	tatgaggatg	960
agaatatg						968

&lt;210&gt; 879

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g729 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 879

atgaaaaaaaa	atgcaagttt	tgaagacttc	tttattctac	ttggattttc	taactggcct	60
catctggaag	tagttctctt	tgtggttate	ttgatcttct	acttgataac	actgatagga	120
aacctgttca	tcatcatcct	gtcatacctg	gactcccatc	tccacactcc	catgtacttc	180
ttcctttcaa	atctctcatt	tctggatctc	tgctacacca	ccagctctat	ccctcagttg	240
ctggtgaatc	tctggggccc	ggaaaagacc	atctcttatg	ctgggtgtac	agttcaactt	300
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ccaccatcag	aaaattctca	agatcaaggc	aagttcattg	ccctctttta	cactgtttgtc	840
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&lt;210&gt; 880

&lt;211&gt; 956

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g730 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 880

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gtcgtggcca	agagtatcct	tctctacctc	attgtggtag	agcacagtct	tcatgcaccc	180
atgttctttt	tcctttccat	gctggccatt	actgatctca	tattgtccac	cacatgtgtc	240
ccccaaaacac	ttagcatctt	ctgggtttgg	ccccaaacag	tttccttggc	tgtctcacc	300
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ttgaccgcta	tatggccatt	tgtcaccctt	tgagatacac	tactattctg	actcccaaaa	420
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agaacagaat	ccttttgctc	tttcccaagg	gggtcccagtg	ataggtgcct	gagctc	956

&lt;210&gt; 881

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g731 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 881

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tctaattggc	ctcatctgga	agtagttatc	tttgtggttg	tcttgatctt	ctacttgatg	120

acactgatag	gaaacctggt	catcatcatc	ctgtcatacc	tggactccca	tctgcacaca	180
ccaatgtact	tcttcctttc	aaacctctca	tttctggatc	tctgctacac	caccagctct	240
atccctcagt	tgctgggtcaa	tctctggggc	ccggaaaaga	ccatctctta	tgctgggtgc	300
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tatgggtgcca	tcgtccgagc	tgtactgagg	atgcagtcaa	ccactgggct	tcagaaaagt	720
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atatatctcc	agccaccatc	aggaaattct	caagatcaag	gcaagttcat	tgccctcttt	840
tatactgttg	tcacacctag	tcttaaccct	ctaattctaca	ccctcagaaa	caaagttgta	900
agaggggagc	tgaagagact	aatgggggtg	gaa			933

&lt;210&gt; 882

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g732 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 882

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tatgtggcca	tatgccaccc	actgtgccat	gctgaagtgc	tcaacagtac	agtaacagcc	120
catattggca	tcgtagctgg	ggtacgggga	tccctctttt	tttccccact	ggctctgctg	180
ataaagacgc	tgggcttatg	ccactcctat	gtgctctcgc	actcctattc	gctccaccag	240
gatgtagcga	acttgtccta	tgcg				264

&lt;210&gt; 883

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g733 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 883

gttgccatct	gtaacccttt	gcgctacctt	acagtcatga	acccccagct	atgcctttgg	60
ttggttcttg	cctgctgggtg	tgggggtttt	atccactcta	tcattgcaggt	catactagtc	120
atccagctgc	ctttctgttg	gccaatgaa	ctggacaact	tctactgtga	tgtcctacaa	180
atcatcaagc	tggcctgcat	ggacacctat	gtggtagagg	tgctgggtgat	agccaacagt	240
ggctctgctg	ctcttgctg	cttcttggtc	ttactattct	cttatgctat	catcctgac	300
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ctgacagtgg	tcagcctgat	cttcgtgcca	tgcgtattca	tctatttgag	gcctttctgc	420
agcttctctg	tggataagat	attctccttg	ttttacacag	tgattacacc	tatgttg	477

&lt;210&gt; 884

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g734 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 884

atgtcagctc	ccaaccactc	cactgccaat	catgatatgt	ttgtcctcat	tggcgcttct	60
ggcctgaagg	agctgcacgt	gtggatctcc	atcccttctt	gtctgatgta	cctgggtggt	120
gtgtcaggaa	atgggtctct	tgtctgtgtg	gtggcagtgg	agcacagtct	tcataaacct	180
atgtaccttt	tcctctccat	gctggcattt	tgggatctga	ttctatccac	atctgcagta	240

cccaaagcct	tgagcatttt	ctggtttgat	gatgtggaca	tctcctttgg	tggtctgtgc	300
actcagctct	tttttatgca	ttttgccttt	gtacgaggat	caggcattct	cttgaccatg	360
gctttcgacc	gctatgtggc	catctgctac	ccattgaggt	atagcaccat	acttagccac	420
agtgttattg	gcaaaattgg	gggtgtcgtg	gtgttcagga	gttttgcaac	tgtcttctcc	480
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tgtgaacaca	tggtgctggc	aaagctaggt	tggtctgaaa	tcaccatcaa	tatttggtat	600
ggaatctctg	taccactact	cagtgttacg	ttagatatgg	tgacaatagt	catctcctag	660
gggctcatag	ttcaagcagt	cttcaggctg	ccctcccttg	gtgcttggat	gaaagcactc	720
agcacctgtg	gttcccatgg	cagtgtcatc	ctcatgttct	gccttccagg	aattttcact	780
gtcatgttgc	agcgctttgc	ctgaaaattt	cccaagtatg	tccacatcct	gctggccaat	840
ctctatgttc	ttgttcccc	catgatgaac	ccaattatct	atggagtaaa	gactaaacag	900
attcagaaag	gggttgcctt	tgtgttttct	ccaaaaggaa	aatgttgc		948

&lt;210&gt; 885

&lt;211&gt; 1087

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g735 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 885

atgccactaa	ctaataaaag	ccaccctgaa	gaattttatc	tgctaggctt	tgcagaccgc	60
ccttggtctag	agcttcctct	gttcactagt	cttcttataa	tgtaccctat	agccgtgatg	120
ggaaacatca	caatcattct	catgtccagg	ttagactctc	gtcttcatag	ccccatgtac	180
tttttctca	ccaacctctc	ctttttggac	atgtgttata	ccacaagcat	tgtccctcag	240
atgctgttta	acctgggaag	ctctaagaag	accatcagct	atatgggggtg	tgcggttcag	300
ctttatttct	ttcacataat	ggggggaaca	gaatgtttgc	ttttggctat	tatgtccttt	360
gatcgctatg	tggtccatctg	cagacctctt	cactacaccc	tcatcatgaa	tcagcgctc	420
tgtatcctta	gtttccaccg	tgtggctaat	tgggaataatc	tatgctgtct	cagaggccac	480
tgccacatta	caattgccac	tgtgtgctct	aataaactgg	accacttggt	gtgtgagatt	540
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gtatgcattt	ttatgttagc	tgtccacta	tgtttaattc	ttgcttcta	tgctagtatt	660
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tcctcccatc	ttattgtagt	tttcttattt	tatggcccag	ccatcagcat	gtaccttcag	780
ccccctcct	ccatctcaag	ggatcaaccc	aagttcatgg	ccctcttcta	tggagtgggtg	840
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cgcaacttgg	tgaggagcat	ttcagcttta	agtgatagtg	ggtagacata	aaatgaagtt	960
attgaacagt	tagagtgggt	tgtctatgggt	ttatctaaca	aattcttgtc	tcataatcaa	1020
atategcttt	acatgttctt	gcaaaatatg	ttatgtctcc	gagactcttt	gtaaacatgt	1080
tcagcaa						1087

&lt;210&gt; 886

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g736 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 886

tttattcatg	ccctctcagc	cattgaatcc	accatcctgc	tggccatggc	ctttgaccgt	60
tatgtggcca	tctgccaccc	actgcgccat	gctgcagtgc	tcaacaatac	agtaacagcc	120
cagattggca	tcgtggctgt	gggtccggga	tccctctttt	ttttcccaact	gcctctgctg	180
atcaagcggc	tggtcttctg	ccactccaat	gtgctctcgc	actcctattg	tgtccaccag	240
gatgtactga	agttggccta	tgcagacact	ttgcccaatg	tggtatatgg	tcttactgcc	300
attctgctgg	ccatgggcgt	ggacgcaatg	ttcatctcct	tgtcctattt	tctgataata	360
cgaacggttc	tgaactgcc	ttccaagtca	tagcgggcca	aggcctttgg	aacctgtgta	420
gtacacattg	gtgtgggtact	cggcttgtat	gtgccactta	ttggcacttc	aagtggctac	480
cggtttggga	acaaactt					498

<210> 887  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g737 nucleotide)

<220>  
 <223> Synthetic construct

<400> 887  
 atgatgatta aaaaaaatgc aagttcggaa gacttcttta ttctacttgg attttctaata 60  
 tggcctcagc tggaaagtagt tctctttgtg gttatcttga tcttctacct gatgacactg 120  
 acaggaaacc tgttcatcat catcctgtca tacgtggact cccatctcca cacaccaatg 180  
 tacttcttcc ttccaacact ctcatctctg gatctctgcc acaccaccag ctctatccct 240  
 cagttgctgg tgaatctccg gggcccgaa aagaccatct cgtatgctgg ttgcatgggt 300  
 caactttact ttgttcttgc actgggaatc gcagagtgtg tctactgggt ggtgatgtcg 360  
 tatgatcgtt atgtagctgt gtgtagacct ttgcattaca ctgtctcat gcacctcgt 420  
 ttctgccact tgttggctgc ggcttcttgg gtaattgggt ttactatctc agcacttcat 480  
 tctctcttta ctttctgggt acccttctgt ggacatcgcc tagtggatca cttcttctgt 540  
 gaagttccag cacttctgcg tttatcatgt gttgacaccc atgcaaatga gctgacctc 600  
 atgggtcatga gctccatttt tgttctcata cctctcatte tgattctcac tgcctatgggt 660  
 gccattgccc gggctgtact gagcatgcaa tcaaccactg ggcttcagaa agtgtttagg 720  
 acatgtggag cccatcttat ggttgtatct ctcttttca ttccagtcac gtgcatgtat 780  
 ctccagccac catcagaaaa ttctcctgat cagggcaagt tcattgccct cttttatact 840  
 gttgtcacac cgagtcttaa tctctaatc tacactctca gaaacaagca tgtaaaaggg 900  
 gcagcgaaga gactattggg gtgggagtg gggaag 936

<210> 888  
 <211> 453  
 <212> DNA  
 <213> Unknown (H38g738 nucleotide)

<220>  
 <223> Synthetic construct

<400> 888  
 cggccgctgt gcgcgccccg cctgctggac cacttcatct gtgagctgcc ggcgttgctc 60  
 aagctggcct gcggaggcga cggagacact accgagaacc agatgttcgc cgcccgctg 120  
 gtcatcctgc tgcgggggggt tgccgtcatc ctggcctcct acggtgccgt ggcccgagct 180  
 gtctgttgca tgcggttcaa cggaggccgg agggaggcgg tgggcacgtg tgggtccac 240  
 ctgacagccg tctgcctgtt ctacggctcg gccatctaca cctacctgca gcccgcgag 300  
 cgctacaacc aggcacgggg caagttcgta tcgctcttct acaccgtgggt cacacctgct 360  
 cttaacccgc tcatctacac cctcaggaat aagaaaatga aaggggcacc gaggaggctg 420  
 ctgcggagtc ttgggagagg ccaggctggg cag 453

<210> 889  
 <211> 1014  
 <212> DNA  
 <213> Unknown (H38g739 nucleotide)

<220>  
 <223> Synthetic construct

<400> 889  
 aaagtcaatg ctagctctga ggggtacttt attttagttg gattttctaa ttggccttat 60  
 ctggaagtag ttctctttgt gggtattttg atcttctgct tgatgacact gataggaaac 120  
 ctgttcatca tcatcctgac gtacctggac tccatctcc atactccctt gtatttcttc 180  
 ctttcaaate tctcatctct ggatctctgc tacaccacca gctctatccc tcagttgctg 240  
 gtcagtctct ggggtgtgga aaagaccatt tcttatgctg gttgcatgggt tcaactttac 300  
 ttttttctca cactgggaac cacagagtgt gtcctactgg tggatgatgc ctatgacctg 360  
 tatgcagctg tgtgtagacc tttgcattac actgtcctca tgcactctcg tttctgccac 420  
 ttgttggtctg tggcttcttg ggtaagtgggt tttaaaacc cagcacttca ttctctcttc 480

accttctggg	tacctctgtg	tggacaccgc	caaataagatc	actttttctg	tgaagttccg	540
gcacttttat	gattatcatt	tgtcaatacc	cgtgaaaata	aactgaccct	catgatcaca	600
agctccat	ttgttctgct	acttctcacc	ctcattttca	cttcctatgg	tgctattgcc	660
caggctgtac	tgaggatgca	gtcaaccact	gggcttcaga	aagtatttgg	aacatgtgga	720
gctcatcata	tggttgtatc	tctctttttc	attccggcca	tgtgcatgta	tctccagcca	780
ccatcaggga	attctcaaga	tcaaggcaag	ttcattgtct	tcttttatac	tggtgttaca	840
cctagtctta	accctcta	ctacaccctc	agaaacaaag	atgtaagagg	ggtagtgaag	900
agactaagg	ggtgggagtg	agcctgtgtt	tgtgtgat	taacaatata	atggagtctt	960
tcctcacaat	gattcatcca	tctgttcatt	tatcaaccat	tcttttat	actc	1014

&lt;210&gt; 890

&lt;211&gt; 656

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g740 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 890

ttgcctgaca	tgcgtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagacagaca	tactcctgag	tgtgatggcc	tatgaccagt	ttgtagccaa	180
atgtcacct	ctatatcatt	cagccatcat	gaaccctgtg	tctgtggctt	tctacttttg	240
ttgtctttt	tttttccctc	agtcttttag	atgccagct	gtacaatttg	attgccttac	300
aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctt	ctgtgaccct	tctcaactcc	360
cccatcttgc	atgttgtgac	accttcaaca	ataacataat	cctgtatttc	cctgatgcca	420
tatttggttt	tcttcccatc	tgcgggacac	ttttctctta	cgataaaatt	gtttcctcca	480
ttctgagggt	ttcatcgtca	ggtgggaggt	ataaagccct	ctccacctgt	gggtctcacg	540
tgtcagttgt	ttgctgagtt	tatggaacag	gcgttggagg	gtacctcagt	tcggatgtgt	600
cattttcccc	cagaaagggt	gcagtgacct	cagtgatgta	cgcggttgtc	accccc	656

&lt;210&gt; 891

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g741 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 891

atgattataa	tttgcaatga	cagccacagt	gatttcatcc	ttctgggctt	ctctaacaag	60
ccacatttgg	agaagatact	ttttggatca	tttttatttt	ttattttttg	actcttgcag	120
gaaatatgg	catagttctt	gtgtccttga	aggatccaaa	actccacatc	cctatgtatt	180
tctttcttct	caacctttcc	ttggtagacc	tctgtttgac	cagcagctgt	gttccacaga	240
tggtgattaa	cttctggggc	ccagaaaaga	ccatcagcta	cattggctgt	gccattcaac	300
tctatgtttt	tttgtggctt	ggggccacgg	aatatgtcct	tcttgttgtc	atggctgtgg	360
attgttatgt	agcagtgtgt	catccactgc	aaaataccat	gatcatgcac	ccaaaacttt	420
gtctgcagct	ggctatcttg	gcatggggga	ctggcttggc	ccagtctctg	atccagtccc	480
ctgccaccct	ccggttaccc	ttctgctccc	agcggatgg	ggatgatgtt	gtttgtgaag	540
tcccagctct	gattcagctc	tccagtaact	atactacct	cagtgaatt	cagatgtcta	600
tcgccagtgt	tgctctctct	gtgatgccct	tgatcattat	cctttctctt	tctgggtcta	660
ttgctaaggc	tgtgctgaga	attaagtcaa	ctgcaggaca	gaagaaagca	tttggcacct	720
gcactcttca	ccttcttgtg	gtttctctct	tttatggcac	tgctcacagg	gtctaccttc	780
aacaaaaaaa	tcactatcct	catgaatggg	gcaaatttct	cactcttttc	tacactgtag	840
taacccaac	tcttaatccc	ctcatctaca	ctctaaggaa	caaggaggta	aaggagacac	900
taataagatt	ggggaggagg	acctgggatt	cccagaataa	ctaacaagg	taacatatgt	960
ttacctttgc	t					971

&lt;210&gt; 892

&lt;211&gt; 651

&lt;212&gt; DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

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atagcagagt	catctcccat	gcaggctgtc	tgacacagat	acctttcttt	gtcctttttg	120
tatgtataga	tgacatgctc	ctgactgtga	tggcctataa	ctgatttggtg	gccatctgtc	180
acccccctgca	ctaccacagtc	atcatgaatc	ctcacctctg	tgtcttctta	gttttggtgt	240
cctttttcct	tagcctgttg	gattcccagc	tgacacagctg	gatttgtgta	cacaactcac	300
cttcttcaag	aatgtggaaa	tctataattt	ttttctgtg	acccatctca	acttctcaac	360
cttgccctgtt	ctgacagcat	catcaataac	atattatgta	ttttagatat	ccctatatatt	420
ggttttcttc	ccatttcagg	gatccttttg	tcttactata	aaattgtctc	ctccattcca	480
agaattccat	cgtcagatgg	gaagtataaa	gccttctcca	cctgtggctc	tcacctggca	540
gttggttgct	tattttatgg	aacagggctt	gtagggtacc	tcagttcagc	tgtgttacca	600
tccccagga	agagtatggt	ggcttcagtg	atgtacactg	tggtcacccc	c	651

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

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ctggccttcc	ctgcagccgg	tctcttctgc	ccttgctctc	ctgtgctacc	tcttgacctt	120
gacgggcaat	tggggcgtg	gtgctgcttg	gcngngnngg	accacgcct	gcanacncac	180
gatgtatgna	ctacttcttc	tgccacctgg	ccttggtaga	cgcgggcttc	actactagcg	240
tggtgcccgc	gctgctggcc	aacctgcgcg	gaccagcgct	gctntgncgc	gcagccactg	300
cacggcccga	gctgtgcgca	tcgctggctc	tgggttcggc	cgaatgcgtc	ctctggcggt	360
gatggctctg	gan					373

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

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ggagataaaa	ccatttcctt	taataattgc	atagttcagt	tatttttctt	cattctcttg	120
ggagtcacag	agttttacct	tctggctgcc	atgtcctatg	accgctatgt	ggccatctgc	180
aagcctctgc	attacttgag	tatcatgaat	cgaagagtct	gcacactgct	tgtttttact	240
tcttggtctg	tttcattctt	aatcatattc	ccagcactca	tgttgctttt	aaagcttgat	300
tactgtaggt	ctaataattat	tgaccatttt	acctgtgatt	attttccact	gctgcaactt	360
gcttggttcag	acacaaaatt	cttagagggtg	atgggatttt	cttggtgctgc	gtttactcta	420
atgttcactt	tggcattaat	atctctgtcc	tacataataca	ttatcagaac	aattttgaga	480
attccttcta	ctagtccagag	gacaaaggcc	ttttccacat	gttcttccca	catgggtgtt	540
atctccatct	cttatggcag	ctgcattttt	atgtacatta	aaccctcagc	aaaagataga	600
gtgtccttga	gcaagggagt	ggcaatacta	aacacctcag	tagccccc		648

<210> 895



<211> 659  
 <212> DNA  
 <213> Unknown (H38g745 nucleotide)

<220>  
 <223> Synthetic construct

<400> 895  
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 cacagcagag tcattctcta tgcaggctgc ctgactcaga tgtctctctt tgccattttt 120  
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatgaccggt ttgtagccat 180  
 ctgtcaccct ctatatcgct cagccatctt gaaccctgtt ttctgtggct tcctagattt 240  
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 tacaaatgac ctgcttcaag gatgtggaaa ttcttaattt cttctgtgac cttctcaaac 360  
 tcccccatct tgcattgtgt gacaccttca ccaataacat aatcatgtat ttccctgctg 420  
 ccatatttgg ttttcttcag atctcgggga cccttttctc ttactataaa attgtttcct 480  
 ccattctgag gggttccatc tcagggtggga actataaagc cttctccacc tgtgggtctc 540  
 acctgtcagt tgtttgctga ttttatggaa caggcgttgg agggtaacct agttcagatg 600  
 tgtcatcttc cctgagaaag gctgcagtgg cctcagtgat gtacatggtg gtcacaccc 659

<210> 896  
 <211> 804  
 <212> DNA  
 <213> Unknown (H38g746 nucleotide)

<220>  
 <223> Synthetic construct

<400> 896  
 atgatggcac tcattttcac agactcccat ctccaaagcc caatgtattt cttcctcaat 60  
 gtcctctcgt ttcttgatat ttgttactct tctgtgtgca cacctaagct cttgggtcaac 120  
 ttcttggtct ctgacaagtc catctctttt gagggctgtg tgggtccagct cgccttcttt 180  
 gtagtgcatt tgacagctga gagcttctct ctggcctcca tggcctatga ccgcttctta 240  
 gccatctgtc aacccttcca ttatggttct atcatgacca gggggacctg tctccagctg 300  
 gtagctgtgt cctatgcatt tgggtggagcc aactccgcta tccagactgg aaatgtcttt 360  
 gccctgcctt tctgtgggccc caaccagcta acacactact actgtgacat accacccctt 420  
 ctccacctgg cttgtgccaa cacagccaca gcaagagtgg tcctctatgt cttttctgct 480  
 ctggtcaccc ttctgectgc tgcagtcatt ctacactcct actgcttggc cttgggtggcc 540  
 attgggagga tgcgctcagt agcagggagg gagaaggacc tctccacttg tgccctccac 600  
 tttctggcca ttgccatttt ctatggcacc gtggttttca cctatgttca gccccatgga 660  
 tctactaaca ataccaatgg ccaagtagtg tccgtcttct acaccatcat aattcccatg 720  
 ctcaatccct tcattctatag cctccgcaac aaggaggtga agggcgctct gcagaggaag 780  
 cttcaggtca acatttttcc cggc 804

<210> 897  
 <211> 949  
 <212> DNA  
 <213> Unknown (H38g747 nucleotide)

<220>  
 <223> Synthetic construct

<400> 897  
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 cttagaggatc aacagttgct ctttgcactg tttctgtcca tgtacctggt caccgttctg 120  
 gggaacctgc tcattatcct ggccatcagc tctgactccc acctccacac ccccaggtac 180  
 ttcttctctt ccaatctgtc cctggctgac atcggtttca cctccaccgc agtccccaag 240  
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 tgaccggtat gtggccatct gtcacccctt gtactactgt gtcaccagga accctgcct 420  
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tctgttggtg	ctgcgggtgt	ccttctgcac	cagttgagtc	attcagcact	tttactgtga	540
gcttgctcag	gtcctcaggc	ttacctgctc	agacacacat	gtcaattaca	tcctgtctcta	600
cgtgggtggcc	ggccttctgg	actttgtgcc	cttctcaggg	atccttttct	cctacaccca	660
aattgtctcc	tacatcctga	gaatctcatc	cacagatggg	aaacacaaag	ccttttctac	720
ctgtggatct	catctgtttg	tggtttcttt	attctatggg	acaggccttg	gtgtgtatct	780
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cctagaaaca	ctgcttgga	gaatgctgta	tgctcaatga	cggggacat		949

&lt;210&gt; 898

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g748 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 898

atggagaatt	gtacggaagt	gacaaagttc	attcttctag	gactaaccag	tgtcccagaa	60
ctacagatcc	ccctctttat	cttggttacc	ttcatctacc	tcctcactct	gtgtgggaac	120
ctggggatga	tgttgctgat	cctgatggac	tcttgctctc	acacccccat	gtacttttct	180
ctcagtaacc	tgtctctggg	ggacttttga	tactcctcag	ctgtcactcc	caagggtcatg	240
gctgggttcc	ttagaggaga	caaggctcatc	tcctacaatg	catgtgctgt	tcagatgttc	300
ttctttgtag	ccttggccac	ggtggaaaat	tacttggttg	cctcaatggc	ctatgaccgc	360
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tcaagcttta	atatcttttt	tgttcttcta	gttatcttta	tctcctactt	gttcattatc	660
atcaccatct	tgaagatgca	ttcagctaaag	ggacacaaaa	aagcattgtc	cacctgtgcc	720
tctcacttca	ctgcagtctc	cgtcttctat	gggacagtaa	tcttcatcta	cttgagccgc	780
agctccagcc	actccatgga	cacagacaaa	atggcatctg	tgttctatgc	tatgatcatc	840
cccatgctga	accctgtggg	ctacagcctg	aggaacagag	aagtccagaa	tgcattcaag	900
aaagtgttga	gaaggcaaaa	atttcta				927

&lt;210&gt; 899

&lt;211&gt; 938

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g749 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 899

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gagcaggagg	agctcagagg	catcctcttt	gtgctcttcc	tgctcatgca	ttcagtcact	120
gttatgggca	acctgggaat	gatcactctg	atccatgcag	accacagct	ccacaccccc	180
atgtattttct	tcctgagcgt	cctatccttc	atagactcct	cgttttccac	agtggacacc	240
cccaggctgc	tggagagctt	cctcatctca	agccaatcca	tctcctttgc	aggctgtatg	300
gtccagatgg	ccctcatgat	cctccatggg	actgctgagt	gtctgctcct	ggccatcatg	360
gcctatgacc	gattcaccgc	catctgccac	cctctcctct	atcacactat	tatatcccaa	420
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cctacatcct	cgtgaccatt	tgcaggatgc	gctccctgca	agcccagagc	aaagctctct	720
ccacctgtgc	ctcccacctc	accatcatct	gcctcttcta	tagcaccatc	accttcattg	780
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ctgtggtcat	cgcagggctg	aacctctctg	ctacagcct	gaggaataaa	gatgtaaaat	900
atgctttgaa	gaggagatgc	ctgtgcaagc	tgtcttca			938

<210> 900  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g750 nucleotide)

<220>  
 <223> Synthetic construct

<400> 900  
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 ctgcagggtc ccctctttat aacgttcccc ttcattctata ttatcactct gggtggaaac 120  
 ctgggaatta ttgtattgat attctgggat tctgtctcc acaatcccat gtactttttt 180  
 ctgagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgctcatg 240  
 gctggattcc ttatagaaga caaggtcac tcttacaatg catgtgctgc tcaaagtgtat 300  
 atctttgtag cttttgccac tgtggaaaat tacctcttgg cctcaatggc ctatgaccgc 360  
 tatgcagcag tgtgcaaacc cctacattac accacaacca tgacaacaac tgtgtgtgct 420  
 cgtctggcca taggtcctca cctctgtggt tctctgaatg cctccatcca cactggggac 480  
 acatttagtc tctctttctg taagtccaat gaagtcacac actttttctg tgatattcca 540  
 gcagtcagtg ttctctcttg ctctgataga catattagcg agcttggtct tatttatgtt 600  
 gtgagcttca atatctttat agctctcctg gttatcttga taccctacac attcattttt 660  
 atcaccatcc taaagatgca ctgagcttca gtataccaga agcctttgtc cacctgtgcc 720  
 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcattga cttacaaccc 780  
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatgggtcatc 840  
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900  
 aaagtgttg agaaggcaaa attgtctgta ggaatggcag tt 942

<210> 901  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g751 nucleotide)

<220>  
 <223> Synthetic construct

<400> 901  
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 aatggcatcc taatttggtg catcctctcc caggcaatcc tgcattgagcc catgtacata 180  
 ttcttatcta tgcctggccag tgcctgatgtc ttgctctcta ccaccaccat gcctaaggcc 240  
 ctggccaatt tgtggctagg ttatagccac atttcccttg atggctgcct cactcaaaaag 300  
 ttcttcattc acttctctt cattcactct gctgtcctgc tggccatggc ctttgaccgc 360  
 tatgtggcca tctgtctccc cctgcgatat gtcacaatcc tcacaagcaa ggtcattggg 420  
 aagatcgtea ctgccaccct gagccgcagc ttcattcatta tgtttccatc catctttctc 480  
 cttgagcacc tgcactattg ccagatcaac atcattgcac acacattttg tgagcacatg 540  
 ggcattgccc atctgtectg ttctgatata tccatcaatg tctgggatgg gttggcagct 600  
 gctcttctct ccacaggcct ggacatcatg cttattactg tttcctacat ccacatcctc 660  
 caagcagtc tccgcctcct ttctcaagat gccgcgtcca aggccctgag tacctgtgga 720  
 tcccatatct gtgtcatcct actcttctat gtcctgccc ttttttctgt ctttgcctac 780  
 aggtttgggtg ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840  
 gtcattcctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900  
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902  
 <211> 994  
 <212> DNA  
 <213> Unknown (H38g752 nucleotide)

<220>  
 <223> Synthetic construct

<400> 902

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ctacaagtc	ccctccttat	catgttccat	ctcatatacc	ttgtcaatgt	gggtggaaac	180
ctggggatga	ttgtttta	tggttgggac	attcatctcc	acactcccat	gtattttttc	240
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ttttttgcag	cccttgccac	tgtggaaaat	tctctcttgg	cctcaatggc	ctatgaccgc	420
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agtcattggc	ctgtcttgct	gtgatagaca	tgtgaatgag	ctagttctca	tttatgtagc	660
cagtttcaat	atcttttctg	ccatcctagt	tatcttgatc	tcctacctat	tcataatttat	720
caccatccta	aagatgcaat	cagcttcagg	ataccagaag	gctttgtcca	cctgtgcctc	780
ccacctcact	gcagtcac	tcttctatgg	gactattatc	ttcatgtact	tacagcccag	840
ctctggtcac	tccatggaca	cagacaaact	ggcatctgtg	ttctatacta	tgatcatccc	900
catgctgaac	cccctgggtc	atagcctgag	gaacaacgaa	gtgaagagcg	cattcaagaa	960
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&lt;210&gt; 903

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g753 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 903

atgtcagatt	ccaacctcag	tgataaccat	cttcagaca	ccttcttctt	aacagggatc	60
ccagggctgg	aggctgccc	cttctggatt	gccatccctt	tctgtgccat	gtatcttgta	120
gcactgggtg	gaaatgctgc	cctcatcctg	gtcattgcca	tgacaatgc	tcttcattgca	180
cctatgtacc	tcttctctg	ccttctctca	ctcacagacc	tggtctcag	ttctaccact	240
gtgcccaga	tgctggccat	tttgtggctc	catgtggtg	agatttctt	tggtggatgc	300
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catgctgtca	taggcagaat	tggtttgtt	gggtattcc	gtagtgtggc	tattgtctcc	480
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tatgggctaa	ctgtggctct	gctggccatg	ggactggatt	ccattctcat	tgccatttcc	660
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aaggagattc	ggagtgcact	tctaaaactg	cttcacctgg	ggaagacttc	aata	954

&lt;210&gt; 904

&lt;211&gt; 989

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g754 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 904

cacatagaac	cagggaatga	tacacagatt	tcagaatttc	ttcttctggg	actttcagat	60
aaaccagaat	tgcagccctt	cctctttggg	ctgttcttct	ccatgtacct	ggcactgtg	120
cttgggaatc	tgctcatcat	cctggccaca	atctcagact	cccacctcca	caccccatgt	180
acttcttctg	ctccaacctg	tcttttgctg	acatctgttt	catctctact	acaatcccaa	240
agatgctcgt	aaacatccag	acacagagca	gagtcacac	ttatgcaggc	tgcatcacc	300
agatgtgctt	ttttgtactc	ttagaagcac	tgagacagct	actcctgacc	gtgatggcct	360
atgaccagtt	tgtggccatc	tgtcaccccc	tgcactacat	ggtcacatg	agccccgtgt	420
tctgtggact	gctggttctg	gcacccctga	tcacatcatg	cccctggctc	tgtggactgc	480

tggttctggc	atcctggatt	atcagtgatc	tggattcctc	attacatagc	ttgatgggtgc	540
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tcattccgct	tgccggttct	gataccttcc	ttaatgacat	ggcgatgtat	tttgcagtag	660
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tcattcagggt	agtgccattc	ttcaggaag				989

&lt;210&gt; 905

&lt;211&gt; 932

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g755 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 905

accacatcta	tagatgataa	tacagaggta	aatgaattca	tatgactagg	actaaccaaa	60
gccccagaac	tacaggtcca	cctctttgtc	ttatttaact	tcattctacct	cttcactctg	120
agtgggaacc	tggggatgat	gctgctgac	ctgctggact	ctcgtctcca	cacttccatg	180
tactttttcc	tcagtaacct	gtctctgggtg	gactttttgt	actcagaaac	tgtcactcca	240
aagatgatgg	ctgggttgct	gatagctcac	aaggctcatct	cctacaatgt	atgtgctgct	300
cagatgttct	tttttgcagt	ctttgtctact	gtggaaagtt	acttcttgac	ttcagtggcc	360
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ccctgtgggt	tatagcctga	gaaacaacga	gggtcaagagt	gcattcaaga	ctgtttgttg	900
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&lt;210&gt; 906

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g756 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 906

atgggggggt	ttgggactaa	catctcaagt	actaccagct	tcactctaac	aggcttccct	60
gagatgaagg	gtctggagca	ctggctggct	gcccttctgc	tgctgctttg	tgctattttcc	120
ttcctgggca	acatcctcat	cctctttatc	ataaagggaag	agcagagctt	gcaccagcca	180
atgtactact	tcctgtctct	tttttctggt	aatgacctgg	gtgtgtctct	ttctacattg	240
cccactgtac	tggctgctgt	gtgttttcat	gccccagaga	caacttttga	tgctgtcctg	300
gcccagacgt	tcttcatcca	cttttctctc	tggacagagt	ttggcatcct	actggccatg	360
agttttgacc	actatgtggc	catctgtaac	ccgctgcgct	atgccacagt	gtcactgat	420
gtccgtgtgg	cccacaatgg	catatccatt	gtcatccgca	gcttctgcat	ggatttccca	480
cttcccttcc	tcctgaagag	actgcctttc	tgtaaggcca	gtgtgggtact	ggccatttcc	540
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tcgaacacat	gtgtgtcaca	tatctatgca	gtgctgatct	tctatgtgcc	tatggttagt	780
gtgtccatg	ttcatcgatt	tgggaggcat	gctcctgaat	atgtgcacaa	gttcatgtct	840
ctttgtacct	gccaatgctc	taccgcaatt	atctattcca	tcaagactaa	ggagattcgc	900
aggagactac	acaagatggt	attgggagct	aagttctgat	cgaag		945

<210> 907  
 <211> 989  
 <212> DNA  
 <213> Unknown (H38g757 nucleotide)

<220>  
 <223> Synthetic construct

<400> 907  
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 gtatttggaa acttgcttat catcctgggt atcattttat gctcccacct ccacacctcc 180  
 atgtacttct ttctctccaa cctgtccttt gtagacatct gttttgcctc caccagggtc 240  
 ccaaagatgc tggtagaatat ccaggcacag agcaaaagtca tcacctctgc aggctgcatc 300  
 acccagatgt actttttcat acattttgta ggattggaca gcttcctcct gactgtgatg 360  
 gcctatgacc ggtttgtggc catctgtcac cccctgtact acacgggtcat catgaaccct 420  
 caactctgtg gattgcttgt tctggtatcc tggatcacaa gtgtcttgca ttccttatta 480  
 catagcttaa tggtagctgca gttgtcctta tgcagagagt tggaaatccc ccactttttc 540  
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 ctctaagaca gtttccctcca tatgtgcaat ctcatcagct caagggaagt ataaggcatt 720  
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 gtaccttagc tcggctgcat cccacaactc acactcaggt gcaatagcct cagtgatgta 840  
 cactgtgggc acccccatgc tgaaccctt catctacagc ctgaggaata aggacataaa 900  
 gagggctctg aagaattctt tgggagggaa actagaaaag ggccagttgt cctagggctg 960  
 aagctatata catgattgca aggtcctaaa 989

<210> 908  
 <211> 960  
 <212> DNA  
 <213> Unknown (H38g758 nucleotide)

<220>  
 <223> Synthetic construct

<400> 908  
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 ggaaacctgc tcatcatcct gaccatcagt tcagactccc acctccacac ccccatgtac 180  
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 atgctggtga atatccaaac acaaagcaaa atgatcactt ttgcaggctg cctcactcag 300  
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 gaccgcttcg tggccatctg ttacccccctg cactacacgg tcatcatgaa cccccggctc 420  
 tgtggactgc tggttctggg gtcctgggtc atcagtgta tgggttcctt gcttgagacc 480  
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 ccttccgaag tcctgaagct ggccgtgttct gacaccttca tcaataacat cgtgatgtgt 600  
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 gtcacccccca tgcgtgaacct cttcatctac agcctgagga acaaggacat gaaggggtca 900  
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<210> 909  
 <211> 981  
 <212> DNA  
 <213> Unknown (H38g759 nucleotide)

<220>  
 <223> Synthetic construct

```

<400> 909
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ggaacctgct cagcatcctg gccgtcagcc ctgactccca cctccacacc cccatgcact      180
tcttcctctg caacctgtcc ttgcctgaca tcgggtttcac ctccaccacg gtccccaaga      240
tgatcgtgga catccaatct cacagcagag tcatctccta tgcaggctgc ctgactcaga      300
tgtctctctc tgccattttt ggaggcatgg aagagagaca tgctcctgag tgtgatggcc      360
tatgaccagt ttgtagccat ctgtcaccct ctgtatcatt cagccatcat gaaccctgtg      420
ttctgtggct tcctggtttt gttgtctttt tttttctcag tcttttagac tcccagctgc      480
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tgtatttccc tgctgccata tttgggtttt ttcccctctc ggggaccctt ttctcttact      660
ataaaattgt ttctccatt ctgagggttt catcatcagg tgggagctat aaagccttcg      720
ccacctgtgg atctcacctg tcagttgttt gctgatttta tggaaacaggc gttggagggt      780
acctcagttc agatgtgtcg tcttccttga gaaagcgtgc agtggcctca gtgatgtaca      840
cagtggtcac ccccatgctg aatcccttga tctacagcct gaaaaacagg gatattaaag      900
gtgtcctgtg gcagccgtgc agccgcacgg cagcacagtc tcctctcaat atcttatctg      960
ttccattcct tttgcaggat g                                     981

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<210> 910

<211> 628

<212> DNA

<213> Unknown (H38g760 nucleotide)

<220>

<223> Synthetic construct

```

<400> 910
tcagtgaagt acttgaatga aagtttccca gaggatttca ttctcatggg ctttgtcaaa      60
tatccatggc tggattttct tctcttctgt gtctcttga ccttctacat gtccacattg      120
ttgggaaata gtgctattat tctggctctt caactagatt cccaacttca tagtcttatg      180
tatttccttc tcaccagtct ttccgtctta tatctctgtt tcaccaccac aacagtacct      240
caaatgctgt tcaatttagg gggcccaaca agaacatcac ttaaataggc tgtatggccc      300
aggcctatgt atttcaactg ctagcctgta ttgaatgtgt ccttcttggc atcgtaggct      360
tagactgcta tgtggctgtc tgtaagcctc caaggtacac tataatcata gaccataagg      420
tctgcctgca actgtccagc actgcttggc taattggctc ggccaattca ctgctgcagt      480
caacaatcac aattcagttg cccctgtaga ggtgtatagc tcagatcttc ctttagttag      540
agtctgtcac ctaacagtct ctaactgtaa caacctttga gatctgtctac agcattctat      600
ctgaggccaa cttcatgctg gggagctc                                     628

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<210> 911

<211> 945

<212> DNA

<213> Unknown (H38g761 nucleotide)

<220>

<223> Synthetic construct

```

<400> 911
atggaaccag aaaagcaaac cgaaatctca gaattcttcc tccagggact ctgagaaaag      60
ccagagcatc agaccctcct cttcacaatg ttctcttcca catacctggg caccatcatt      120
ggaaatgcc tcatatcctt ggccatcatc acggactctc acctccacac acccatgtac      180
ttctttctct tcaacctctc actcgttgac accctattat cctccaccac cgtccccaag      240
atgctagcga acatccaggc tcagagcaga gccatccctt ttgtgggctg cctcaccag      300
atgtatgcct tcacctgtt cgggaccatg gacagcttct tcctggcagt aatggccatc      360
gaccgcttcg tggccattgt ccaccacag cgttacttgg ttctcatgtg ctcccctgtc      420
tgtggctgc tgctgggagc atcatggatg atccaacac tccagtctct catacacacc      480
tgctcatgg ctcaactgac cttctgcgcc ggctctgaaa tctccactt cttctgtgac      540
ctcatgccc tgctgaagct ctccggctca gacacgcaca ccaacgagct ggtgatcttt      600
gcttttggca ttgtcgtggg caccagccca ttctcttga tccttctctc gtacatccgc      660

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atcttctgga	cagtctttaa	gatcccttct	actcggggca	agtggaaagc	cttctccacc	720
tgtggcttac	acctcactgt	ggtgtcactg	tcctatggga	ccatctttgc	tgtgtactta	780
cagcccatat	ccccagctc	ctcccagaag	gacaaggcag	ccgccctaata	gtgtgggggtg	840
ttcatcccca	tgctcaaccc	ctttatctac	agcatacgga	acaaggatat	gaaggcagcc	900
ctgggggaagc	tcatcgga	agtggccgctc	ccctgtccta	ggcca		945

&lt;210&gt; 912

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g762 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 912

atgggtccga	ccaacctcac	atctgcccc	gtgttctctc	tcctcggcct	ggtggacgga	60
acagacgccc	acccgctgct	gttctgtctc	tgccttggca	tctatctget	caacgccttg	120
agcaacctga	gcatgggtggc	gctgggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcacctgag	cctcgtggac	gtctgtctta	ccaccgtcac	ggtccccagg	240
ctgctggccg	gcctgtctca	ccggggccag	gccatatacct	tccaggcgtg	ctttgccgag	300
atgtacttct	tctgtgctct	gggcatacacc	gagagctacc	tcctggcggc	catgtcctac	360
gaccgcgcga	cggcggcgtg	ccggccccctg	cgctacggcg	cgctgggtgac	gccatgggcg	420
tgcgcctcgc	tgggtcgtgc	gtcgtgggccc	gtgacgcacc	tgcactcgtc	gctgcacacg	480
ctgctcctct	ccgcgctctc	ctaccctctac	cccacccccg	tgcgccccctt	cttttgcgac	540
atgacggtga	tgctgagctt	ggcgacctcg	gacacgtccg	ccgcgggagac	ggccatcttc	600
tccgagggcc	tggccgtggt	gttggccccg	ctgctcctcg	tgctcctttt	cctacgcgcg	660
catcctggtc	gcggtgctcg	gcttgcccg	gccggcgccg	cgcttctctc	tactgccccg	720
cccacctagt	ggcggtggcg	gtggcgcttt	tctttggctc	tgctctctcc	gtgtatttcc	780
cgcgctcgtc	tgcctactca	gcccgtctac	accgcctggc	cagcgtgggtc	tacgctgtca	840
tcacgcgcgac	cttgaacctc	ttcatcaaca	cgcctcgcaa	caaagagggtc	aagggcgccc	900
tgaaaagggg	gctcagatgg	agggctgcac	cccaagaggc	gtgagggca		949

&lt;210&gt; 913

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g763 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 913

atggatggag	agaatcactc	agtggatatc	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgacctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtggtgtg	gagatgggtc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcctttcat	ttctggctgt	tgcctggacc	cttgggtgtc	gtcactccct	gttccaactg	480
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cttctcggc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggctact	600
gttaacagtg	ggttttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgtttggaa	acattcctca	ggtggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttggtc	tttggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagagg	atctca			936

&lt;210&gt; 914

&lt;211&gt; 954

&lt;212&gt; DNA



<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

atgtggcaga	agaatcagac	ctctctggca	gacttcatcc	ttgaggggct	cttcgatgac	60
tcccttacct	accttttccct	tttctccttg	accatgggtg	tcttccttat	tgcggtgagt	120
ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttcctgctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaac	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaaccagg	300
cacttcctct	atttgtgtct	aggtgggtgct	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcatccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcacttccc	tttctgtggg	cctcggaaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagtt	ggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
atcagcagca	ttctcctcct	cctccccatc	ttcctgattt	ctacatccta	tgtcttcatc	660
cttcaaagtg	tcattcagat	gcgctcatct	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacggtggg	ttctctttgg	tttgggtgcct	gcactttctc	ctacatgaga	780
cccagggtccc	agtgcactct	attgcagaac	aaagttgggt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tgttatcacc	cagtgcattc	aacgactgca	attg	954

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

acgctgtgcg	ccacagcctn	gctgggccac	ttcatctgtg	agctgccggc	gttgcctcaag	60
ctggcccgcg	gagcatcgga	gacactaccg	agaaccagat	gttcgcccgc	cgcgtgggtca	120
tectgtctgt	gccgtttggc	gtcatcctgg	cctcctacgg	tgccgtggcc	gagctgtctg	180
ttgtatgcgg	ttcagcggag	gccggagagg	gcggtgggca	cgtgtgggtc	ccactgacag	240
ccgtctgcct	gttctacggc	tcggcatcta	cacctacctg	cagcccgcgc	agctaacaac	300
caggcacgg						309

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

attcatgccc	tctcagccat	tgaatccacc	atcctgctgg	ccatggcctt	tnaccgttat	60
gtggccatct	gccaccact	gcgccatgct	gcagtgtctca	acaatacagt	aacagcccag	120
attggcatcg	tggctgtggt	ccgcggatcc	ctcttttttt	tcccactgcc	tctgtctgac	180
aagcggctgg	ccttctgcc	ctccaatgtc	ctctcgcact	cctattgtgt	ccaccaggat	240
gtaatgaagt	tggcctatgc	aagacanttt	gcccaatgtg	gtatatggtc	ttaactgncc	300

attttggttg gtc

313

&lt;210&gt; 917

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g767 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 917

atggaaacag	gaaatcaaac	acatgcccaa	gaattttctcc	tcctgggatt	ttcagcaacg	60
tcagagattc	agttcattct	ctttgggctg	ttcctctcca	tgtacctagt	cactttcacc	120
gggaacctgc	tcatcatcct	ggccatatgc	tcagactccc	acctccacac	ccccatgtac	180
ttcttccctc	ccaacctgtc	ttttgctgac	ctctgtttta	cctccacgac	tgtcccaaag	240
atgttactga	atatactgac	acagaacaaa	ttcataacat	atgcaggctg	tctcagtcag	300
atTTTTTTTT	tcaattcatt	tggatgcctg	gacaatttac	tcttgaccgt	gatggcctat	360
gaccgcttcg	tggecgtctg	tcacccccctg	cactatacgg	tcatcatgaa	ccccagctc	420
tgtggactgc	tggttctggg	gtcctgggtg	atcagtgtca	tgggttccct	gtcagagacc	480
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ctacttgaag	tcctgaagct	cgctgtttct	gacaccttca	ttaataacgt	ggtgatatac	600
tttgcaactg	gcgtcctggg	tgtgatttcc	ttcactggaa	tatttttctc	ttactataaa	660
attgttttct	ctatactgag	gatttcctca	gctgggagaa	agcaciaaagc	gttttccacc	720
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agttctgcag	ccacaccatc	ttctaggaca	agtcgtggtg	cctcagtgat	gtacaccatg	840
gtcaccccca	tgtgaacctc	cttcatctac	agcctgagga	acacggacat	gaagagggcc	900
ctggggagac	tcctcagtag	ggcaacattt	tttaatgggtg	acatcactgc	aggactttca	960

&lt;210&gt; 918

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g768 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 918

atgggggaca	accaatcacg	ggtcacagaa	ttcctccttg	ttggattcca	gtcagtggtg	60
gagatggaag	tgtcctctct	ctggatcttc	tcctgtttat	atctcttcag	cctgctggca	120
aatggcatga	tcttggggct	catctgtctg	gatcccagac	tgcgcacccc	catgtacttc	180
ttcctgtcac	acttggccgt	cattgacata	tactatgctt	ccagcaattt	gctcaacatg	240
ctggaaaacc	tagtgaaaca	caaaaaaaaa	tatctcgttc	atctcttgca	ttatgcagat	300
ggctttgtat	ttgacttttg	ctgctgcagt	gtgcatgatt	ttggtggtga	tgtcctatga	360
cagattttgtg	gcgatctgce	atccccctgca	ttacactgtc	atcatgaact	ggagagtgtg	420
cacagtactg	gctattactt	cctgggcatg	tggattttcc	ctggccctca	taaattctaat	480
tctccttcta	aggctgccct	tctgtgggcc	ccaggagggtg	aaccacttct	tcggtgaaat	540
tctgtctgtc	ctcaaaactgg	cctgtgcaga	cacctggatt	aatgaaattt	ttgtctttgc	600
tggtggtgtg	tttgtcttag	tcgggccccct	ttccttgatg	ctgatctcct	acatgcgcac	660
cctcttggcc	atcctgaaga	tccagtcaaa	ggaggggccgc	aaaaaagcct	tttccacctg	720
ctcctcccac	ctctgtgtgg	ttgggcttta	ctttggcatg	gccatggtgg	tttacctggt	780
cccagacaac	agtcaacgac	agaagcagca	gaaaattctc	accctgtttt	acagcctttt	840
caaccatttg	ctgaaccccc	tcatctacag	cctgcggaat	gctcaagtga	aggggtgcctt	900
atacagagca	ctgcagaaaa	agaggaccat	gtgaatg			937

&lt;210&gt; 919

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g769 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 919

atggaaccag	gaaatgatac	acaaatttca	gaatttcttc	ttctgggatt	ttcacaagaa	60
cctggactgc	aacccttcct	ctttgggctg	ttcctgtcca	tgtacctggt	cactgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
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gtcaccccca	tgctgaacct	ctttatctat	agtctgagga	ataaagacat	aaagagggct	900
ctgggaatac	atttgttgtg	gggaacaatg	aaagggaat	ttttcaagaa	gtgcccc	957

&lt;210&gt; 920

&lt;211&gt; 222

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g770 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 920

ggagacacta	cagagaacca	gatgttcgcc	gcccgcgtgg	tcatcctgct	gctgccgtat	60
gacgtcatac	tggcctccta	aggtgccgtg	gcccagagctg	tctgttgcac	gcggttcagc	120
ggaggaccga	ggagggcgt	gggcacgtgt	gggtcccacc	cgacagccgt	ctggctgttc	180
taaggctcgg	gcaaataaac	ctatctgcaa	gccgcgcagc	ta		222

&lt;210&gt; 921

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g771 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 921

atgaaatcat	ggaacaatac	aataatttta	gaatttcttc	tcctgggaat	ttcagaggaa	60
ccagaattgc	aggccttctc	ctttgggctg	ttcctgtcca	tgtacctggt	cactgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	cttcgtaggc	atctgttttg	tctctaccac	tgtcccgaag	240
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atgtgctttt	tcttactctt	tgtaggattg	gataacttcc	ttctgaccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctctg	cactacatgg	tcattatgaa	ccctcaactc	420
tgtggactgc	tggttctggc	atcctggatc	atgagtgttc	tgaattccat	gttacaaagc	480
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attaatcagg	tggtccacct	tgcctgttct	gacaccttcc	ttaatgacat	agtgatgtat	600
ttcgcagtag	cgctgctggg	cggtgttccc	ctcactggga	tcctgtactc	ttactctaag	660
atagtttctc	ccatacgtgc	aatctcatca	gctcagggga	agtataaggc	attttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatggtg	catgcttagg	ggtgtacctt	780
agttctgctg	ccaccacaaa	ttcacacaca	ggtgctgcag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgctgaacct	cttcatctac	agtctgagga	ataaacacat	aaagggtgct	900
atgaaaacat	tcttcagagg	aaagcaa				927

&lt;210&gt; 922

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g772 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 922

atggtcacag	agttcctccc	actgggattt	ctcctggggc	caaggattca	gatgctcctc	60
cttgggctct	tctccctggt	ctatgtcttc	accccgctgg	ggaatgggac	catcccgggg	120
ctcatctcac	tggactccag	actccacacc	cccatgtact	tcttctcttc	acacctggcc	180
gtcgtcaaca	tgcctatgc	ctgcaacaca	gtgccccaga	tgctggtgaa	cctcctgcat	240
ccagcc						246

&lt;210&gt; 923

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g773 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 923

ctcatggacc	tcaagctcat	ctgcaccacc	gtacccaaga	tggccttcaa	ctacctgtct	60
ggcagcaagt	ccattttctat	ggctgggtgt	gtcacacaaa	ttttcttcta	tatatcactg	120
tctggctctg	aatgttttct	tttggctgtt	atggcttatg	accgctatat	tgctatttgc	180
cacctcttaa	gatataccaa	tctcatgaat	cctaaaattt	gtggacttat	ggctaccttc	240
tcttggatcc	tgggctctac	agatgggaatc	attgatgctg	tagccacatt	tcccttctcc	300
ttttgtgggt	ctcgggaaat	agcccacttc	ttctgtgaat	tcccttccct	actaatcctc	360
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gttttccctg	ttgcaatcat	cattgcttcc	tatgctcgag	ttattctggc	tgtcattcac	480
atgggatctg	gagagggtcg	ttgcaaagct	ttcacgacct	gttctcttca	cctcatggtg	540
gtgggaatgt	actatggagc	agctttgttc	atgtacatac	ggcccacatc	tgatcactcc	600
ccaacgcagg	acaagatggt	gtctgtattc	tacaccatcc	tactccc		648

&lt;210&gt; 924

&lt;211&gt; 916

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g774 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 924

atgaaaccag	ggaatgatac	acgaatttca	gaattttcttc	ttctaggact	ttcagcagaa	60
ccagaattgc	agcccttctt	ctttgggctg	ttcctgtcca	tgtacctggt	caccgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ctttgcagat	atcagttttg	tgtctaccac	tgtcccgaag	240
atgctggtga	atatccagac	gcagagcaga	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	tcctactatt	tgcagtgttg	gacagccttc	tcctagctgt	gatggcctat	360
gatcggtttg	tggccatctg	tcctcctctg	tactacacaa	tcatcatgaa	ccctcagttc	420
tatagactgg	attcttagtg	tcctgaattc	tctgttacaa	agcttaatgg	tgttgccact	480
gcccttctat	acagacatag	caatccccca	ctttttctgt	gaacttaatc	agataatctg	540
cattgcctgt	tctgacacct	ttcttaatga	catcatgata	tattgtgcaa	ctgtgctgct	600
gggcggtggt	cccctcactg	gaatccttta	ctcttactct	aagatagttt	cctccatacg	660
tgcaatctca	tcagctcagg	ggaagtacaa	ggcattttcc	acctgtgcat	ctcacctctc	720
agttgtctcc	ttgttttatg	gtacaagcct	aggaatgtac	cttagttctg	ctgcaaccca	780
caactcacc	tcaagtgcaa	cagcctcagt	gatgtacact	gtggtcaccc	ccatgctgaa	840
cccctttatc	tacagtctga	ggaataaaga	cctaaaggat	gctctgaaac	gcttcttcag	900
aaggaaagcaa	taaaag					916

&lt;210&gt; 925

<211> 360  
 <212> DNA  
 <213> Unknown (H38g775 nucleotide)

<220>  
 <223> Synthetic construct

<400> 925

ttttcctct	cacacctggc	gggtgttgac	attgcctacg	cctgcaaacac	gggtgccccgg	60
atgctgggtga	acctcctgca	tccagccaag	cccattctct	ttgcggggccg	catgatgcag	120
acctttctgt	tttccacttt	tgctgtcaca	gaatgtttcc	tcctgggtggt	gaagtccaat	180
gatttgtagc	tggccatctg	ccacccctcc	cgatatttgg	ccatcatgac	ctggagagtc	240
tgcatcacc	tcgcggtgac	ttcctggacc	actggagtc	ttttatcctt	gattcatctt	300
gtgttacttc	tacctttacc	cttctgtagg	ccccagaaaa	tttatcactt	tttttgtgaa	360

<210> 926  
 <211> 643  
 <212> DNA  
 <213> Unknown (H38g776 nucleotide)

<220>  
 <223> Synthetic construct

<400> 926

ttgcctgaca	tcgggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	atccaatctc	60
acagcagagt	catctcctat	gcaggctgcc	tgactcagat	gtctctcttt	gccatttttg	120
gaggcatgga	agagagacat	gctcccagat	gtgatggcct	atgaccgggt	tgtagccatc	180
tgtcaccctc	tatatcatte	agccatcatg	aaccggtgtt	tctgtggcct	cctagttttg	240
ctgtcttttt	tttctttctt	tttctcagct	gcacaacttg	attgccttac	aaatgacctg	300
cttcaagaat	gtgggaattc	ctaatttcct	ctgtgaccct	tctcaactcc	cccattctac	360
atgttgtgac	accttcacca	atcacataat	catgtatttc	cccgttgcca	tatttggttt	420
tcttcccatc	tcgggggacc	ttttctctta	ccatgtaatt	gtttcctcca	ttctgagggt	480
ttcatcatca	ggtgggaagt	ataaagcctt	ctccacctat	gggtctcacc	tgtcagatgt	540
ttcctgattt	tatggaacag	gcgttggagg	gtacctcagt	tcagatgtgt	catcttcccc	600
gagaaagact	gcagtggcct	cagtgatgta	cgcagtggtc	acc		643

<210> 927  
 <211> 498  
 <212> DNA  
 <213> Unknown (H38g777 nucleotide)

<220>  
 <223> Synthetic construct

<400> 927

gtgaaaaatc	agacaatggt	cacagagttc	cttctatttg	gatttttcct	gagcccaagg	60
atacacatgc	tcctcttttg	gctctttctac	ctgttctatg	tcttcaccct	gctggggaat	120
gggaccatcc	tggggctcat	ttcactggac	tccatactcc	acaccccat	gtacttcttc	180
ctataacacc	tgctcgtcgt	caacatcgcc	tatgcctgca	acacagtgcc	ccagatgctg	240
gtgaacctcc	tgcatcagc	caagccatt	tactttgctg	gctgcatgac	atataccttt	300
ctctttttga	gatttgacac	tactgaatgc	ctcctgttgg	tgctgatgtc	ctacgattgg	360
tacgtggcca	tcttgacacc	tctccgatat	atcatcatta	tgacctgtaa	agtcttcac	420
atctctgcca	tcactttcat	gtacatgtgg	ttcctttctg	tcttgggtcca	tgtaagcctc	480
atactaagac	tgcctttt					498

<210> 928  
 <211> 276  
 <212> DNA  
 <213> Unknown (H38g778 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 928

caaatgagct	tgtttgtaat	ctttgcctct	ggctgaatgc	aatttgttta	aactcgcaact	60
ggcctataga	cccctgttac	tgccatctgt	gcacccaccc	gttctaccac	attgaccatg	120
tctaagaggc	cattatcttt	ttcttggttag	caggatgcta	ccttggtggg	ttagttaaga	180
tggtcactgt	gacaacttcc	atcacacaac	tatcgctttg	tcaacccatgt	gtccacctgc	240
cttctctgtg	acattccctc	atttttagtc	tattcg			276

&lt;210&gt; 929

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g779 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 929

ttctctgatc	tctgcttttc	ctctgtcaca	atacctaaat	tgcttcagaa	catgcagagc	60
caagtaccaa	cgatataccta	tgcagattgc	ctgacacagc	tgtacttctt	tatgggtttt	120
ggagatatgg	agagcttcct	tcttgtggtc	atggcctatg	accgctatgt	ggccatctgc	180
ttccctttgc	attataccag	catcatgagc	accaaatttt	gtgctttact	agtgtacta	240
ctgtggatgc	tgacaatatc	ccatgccctg	ctgcataccc	tactcatggc	tagattgtct	300
ttttgtgaga	agaatgtcat	tcttcacttt	ttctgtgata	ttctgtctct	tctgaagttg	360
tcctgctcag	acacttatgt	taatgagttg	atgatattta	tcatgggagg	gatcatcagt	420
attattccat	ttctactcat	tgttatgtct	tatgtaagga	ttttttcttc	cattctcaag	480
gttccatctt	ctcaggacat	ccacaaggtc	ttctctacct	gtgggtccca	tctgtctgtg	540
gtgaccttgt	tttatgggac	aattattggg	ctctacttat	gtccatcagg	caataattct	600
actgtgaatg	agattttccat	ggccatgatg	tacacagtgg	tggt		645

&lt;210&gt; 930

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g780 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 930

agcaacctat	ccttcactga	cctctaattt	tcctctgtca	caatgcccaa	gttgctgcag	60
aacatgcaga	gccaagttcc	ttcaatcccc	tatgcaggct	gcctgacaca	aatgtacttc	120
cttttgtttt	ttggagatct	tgagagcttc	ctccttgtgg	ccatggccta	tgaccgctat	180
gtagccatct	gcttccctct	tcattacacc	agcatcatga	gccccaggct	ctgtgtgagt	240
cttgtgtgc	tgtcctgggt	gctgaccatg	tcccattcca	tgctgcacac	tttgctctta	300
actaggttgt	ctttctgtga	aaacaatgtg	atccccatt	ttttctgtga	tctgtctgcc	360
ctgctgaagc	tggcctgctc	tgatattcac	attaatgaat	tgggtgatatt	gatcatagga	420
gggcttggtg	ttatacttcc	atttctactc	atcacagtgt	cttatgcacg	catcatctcc	480
tccattctca	agggtccctc	aactcaaggc	atccacaagg	tcttctccac	ttgtgggtct	540
cacctgtctg	tgggtgtcact	gttctatggg	acaattattg	gcctctactt	atgtccatct	600
gctaataact	ctactctaaa	ggacactgtc	atgtctatga	tgtacaccgt	ggttaact	657

&lt;210&gt; 931

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g781 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 931

atggagaaca	acacagaggt	gactgaattc	atccttgtgg	ggttaactga	tgaccagaa	60
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ctgcagatcc	cactcttcat	agtcttcctt	ttcatctacc	tcatactct	ggttggaac	120
ctggggatga	ttgaattgat	tctactggac	tcctgtctcc	acaccccat	gtactcttc	180
ctcagtaacc	tctccctggg	ggactttggt	tattcctcag	ctgtcactcc	caaggatg	240
gtggggtttc	tcacaggaga	caaattcata	ttatataatg	cttgtgccac	acaattcttc	300
ttctttgtag	cctttatcac	tgcagaaagt	ttcctcctgg	catcaatggc	ctatgaccgc	360
tatgcagcat	tgtgtaaacc	cctgcattac	accaccacca	tgacaacaaa	tgtatgtgct	420
tgccctggcca	taggctccta	catctgtggt	ttcctgaatg	catccattca	tactgggaac	480
actttcaggc	tctccttctg	tagatccaat	gtagttgaac	actttttctg	tgatgctcct	540
cctctcttga	ctctctcatg	ttcagacaac	tacatcagtg	agatgggtat	ttttttgtg	600
gtgggattca	atgacctctt	ttctatcctg	gtaatcttga	tctcctactt	atttatattt	660
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tcccacctta	ctgcagtttc	catcttttat	gggacaggaa	tctttatgta	cttacgacct	780
aactccagcc	atttcatggg	cacagacaaa	atggcatctg	tgttctatgc	catagtcatt	840
cccattgtga	atccactggg	ctacagcctg	aggaacaaa	agggttaagag	tgcccttaaa	900
aagactgtag	ggaaggcaaa	ggcctctata	ggattcatat	tt		942

&lt;210&gt; 932

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g782 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 932

gcaacaaagg	agctgtgttt	tcttggggta	tatattccca	aaggcgatgc	ctgctggaaa	60
tgactcctct	gggcctgcat	ttactcttgc	taggttgaca	agttgtctcc	atgggtgggga	120
acctggcctt	gattgctcta	attggctgaa	attcatacct	tcccaccccc	aagctctgtt	180
ttctttcacc	cagtccttcc	ctgatctcta	ttgtcctgtt	tgacccccca	gaatgctcat	240
gacttttcta	tcaaagaaaa	acatcttcta	tgacaggtgc	atgactcagc	tgctgcagct	300
tttctttctc	tttattgtcc	tactctatta	aataccacgt	gttgatgttc	atagcctgtg	360
gttgcttagt	ggccatctac	aatccatcat	tgcatgaggt	caccatgtct	cctcaggtga	420
gagagagaga	gagagtggat	ttgctggaac	cactcccaca	cagggcacat	acttaggccg	480
aacttgtgta	atattgatgt	catcaatcat	catcttatga	cagcctcttg	gtcctctaag	540
tttctgttac	cagcacctgt	gc				562

&lt;210&gt; 933

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g783 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 933

atgactgggg	gaggaaatat	tacagaaatc	acctatttca	tcctgctggg	attctcagat	60
tttcccagga	tcataaaaagt	gctcttcact	atattcctgg	tgatctacat	tacatctctg	120
gcctggaacc	tctccctcat	tggttttaata	aggatggatt	cccacctcca	tacacccatg	180
tatttcttcc	tcagtaacct	gtccttcata	gatgtctgct	atatcagctc	cacagtcccc	240
aagatgctct	ccaacctctt	acaggaacag	caaactatca	cttttggttg	ttgtattatt	300
cagtacttta	tcttttcaac	gatgggactg	agtgagtctt	gtctcatgac	agccatggct	360
tatgatcggt	atgctgccat	ttgtaacccc	ctgctctatt	catccatcat	gtcaccacc	420
ctctgtgttt	ggatgggtact	gggagcctac	atgactggcc	tcactgcttc	tttattccaa	480
attgggtgctt	tgcttcaact	ccacttctgt	gggtctaatg	tcatacagaca	tttcttctgt	540
gacatgcccc	aactgttaat	cttgctcctgt	actgacactt	tctttgtaca	ggtcatgact	600
gctatattaa	ccatgttctt	tgggatagca	agtgccttag	ttatcatgat	atcctatggc	660
tatatgtgca	tctccatcat	gaagatcact	tcagctaaag	gcaggccaaa	ggcattcaac	720
acctgtgctt	ctcatctaac	agctgtttcc	ctcttctata	catcaggaat	ctttgtctat	780
ttgaggtcca	gctctggagg	ttcttcaagc	tttgacagat	ttgcatctgt	tttctacact	840
gtggtcattc	ccatgttaaa	tcccttgatt	tacagtttga	ggaacaaaaga	aattaaagat	900
gccttaaaaga	ggttgcaaaa	gagaaagtgc	tgc			933

<210> 934  
 <211> 935  
 <212> DNA  
 <213> Unknown (H38g784 nucleotide)

<220>  
 <223> Synthetic construct

<400> 934  
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 ttccaaaga accctatddd cctcttttca atattcctag ggatctacct cctgacagtg 120  
 tcctggaaca taaacctcat cacccttatc aggacgactc ccatctgcat acacctatgt 180  
 actttttcct tagtaatctg tcgtttctgg acatctgcta tgtttccact atagccccc 240  
 agatgctctc agacttcttc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300  
 agtacttttt cttctctagc ctaggctctaa ctgagtgtg tcttctggca gccatggctt 360  
 atgatcgata tgctgccatt tgcaaccctc tgctctacag ggccatcatg tttcccaccc 420  
 tctgctgca gatgggtggca ggatcttgta taactggatt cttaggctca tttatccaac 480  
 tctgtgcctt gcttcagctc catttctgtg ggccaaatgt catcaaccat ttcttctgtg 540  
 atctgcccc gctgctgatt ctatcctgtt ctgacacctt tttctttcaa gtcatgacct 600  
 ctgttctcac agtgatcttt ggactcacgt ctgtcttagt tatcatgata tcttatggtt 660  
 atatcattgc caccattctg aagatcacct cagctgaagg cagagccaaa tctttcaaca 720  
 cttgtgcttc tcacctaca gcagtgatcc ttttcttgg ctcaggtatc tttgtttata 780  
 tgtatcctaa tgctgggtgat tccctgagcc aaaacaagt ggcatcagtc ttatacacag 840  
 ttacaatccc catgttaaat ccagtgatct acagcctgag gaacaaggaa atcaaatgatg 900  
 ctctaaacag atggaagaag agaattcttct cctgg 935

<210> 935  
 <211> 1330  
 <212> DNA  
 <213> Unknown (H38g785 nucleotide)

<220>  
 <223> Synthetic construct

<400> 935  
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 tattcaaaga ccactatddd tctcttttca gtattcctag ggatataacct cctgaccatg 120  
 tcctgaaacg tgagtctcat cgcccttatc aggacggact cccatctaca tgcacctgtg 180  
 tactttttcc ttagtaatcc gtcttttctg gacatctgct gtgtttccac tatagcccc 240  
 aagatgccct cagacttttt caagaagcat aaattcattt cctttatggg gtgcaccatg 300  
 cagtacttct ctagcctgaa tgtgactgag tgctgtcttc ttacagccat ggcttatgat 360  
 taatatgctg ccatttggtga tctctgtctc tacacagcca tcatgtcacc tgctctctgt 420  
 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480  
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgccc 540  
 caactgctga ttctatcctg ttctcatact gttttttttt tctcaagtca tgaccactat 600  
 gctcacagta acctttatac tcacctctat cttgggtatc atgataactt atgggtatat 660  
 cattgccaac attcatctct tttatgggat gcaccatgta atacttcttc tctagcctgg 720  
 gtctgactga gtgctgtctt ctggaagcta tggcttataa ttgatatgct gccatttgtg 780  
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 cctgtataac tattatcttt ggctcattta tccaactatg tgctttgctt cagctccatt 900  
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 gctatgacac ctttttctgt caagtcatga catccatgct tacagtggta tttggactca 1020  
 catctgtctt agttatcatg atattttatg gctatgtcat tgctaccatt ctgaagatca 1080  
 tctcagttga aggcaggtct aaggtcttca acactgggtg ttctccctga tagcagtgc 1140  
 tctcttctat tgctcaagaa tctttgtcta tatgtgctct cactctgatg cttctctgag 1200  
 tagaaacaag gtggattcta ttgtatacac tgtgggtgat cccaggttga atccattgat 1260  
 ctacagcctg agtgacaagt aaatcaaaga tgccttaaag agatggacga agagaatatt 1320  
 ctctggcct 1330

<210> 936



<211> 930  
 <212> DNA  
 <213> Unknown (H38g786 nucleotide)

<220>  
 <223> Synthetic construct

<400> 936  
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 aggattcaga tgctcctctt tgggctcttc tccctgttct atatcttcac cctgctgggg 120  
 aacggggcca tcttgggggt catctcactg gactccagac tccacacccc catgtacttc 180  
 ttctctctac acctggctgt cgtcgacatc gcctacaccc gcaacacggg gccccagatg 240  
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 tttctctgtt tgagtttttg acacagcgaa tgtctcctgc tgggtgctgat gtcctacgat 360  
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 ctcatcctaa gactgccctt ctctgggctt catgaaatca accacttctt ctgtgaaatc 540  
 ctgtctgttc tcaggctggc ctgtgctgac acctggtcca accagggtgg catctttgca 600  
 gcctgcgtgt tcttctctgt gggggcaccg agcctgggtg ttgtctccta ctgcacatc 660  
 ctggcgggca tcttgaggat ccagtctggg gagggccgca gaaaggcctt ctccacctgc 720  
 tcttcccacc tctgcgtggg gggactcttc tttggcagtg ccatcatcat gtacatggcc 780  
 cccaagtccc gccatcctga ggagcagcaa aaggctcttt ttctatttta cagttttttc 840  
 aacccaacac ttaacccctt gatttacage ctgaggaacg gagaggtcaa ggggtgccctg 900  
 aggagagcac tgggcaagga aagtcattcc 930

<210> 937  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g787 nucleotide)

<220>  
 <223> Synthetic construct

<400> 937  
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 cctgagctcc aggggcagct ctttgtgggt ttcttggtta tttatctggt gaccctgata 120  
 ggaaatgcca ttattatagt catcgtctcc ctgaccaga gcctccacgt tcccatgtac 180  
 ctgtttctcc tgaacttate tgtgggtggc ctgagtttca gtgcagttat tatgcctgaa 240  
 atgctgggtg tctctctac tgaaaaaact acaatttctt ttgggggctg ttttgacag 300  
 atgtatttca tcttctttt tgggtggggt gaattgtttc ttctgggagc aatggcttat 360  
 gaccgatttg ctgcaatttg ccatcctctc aactaccaa tgattatgaa taaaggagtt 420  
 tttatgaaat taattatatt ttcattgggc ttaggtttta tgtaggtac tgttcaaaca 480  
 tcatgggtat ctagtgttcc ctttgtggc cttaatgaaa ttaaccatat atcttgtgaa 540  
 acccagcag tgttagaact tgcattgtga gacacgtttt tgtttgaaat ctatgcattc 600  
 acaggcacct ttttgattat tttgggtcct ttcttggtga tactctgtc ttacattcga 660  
 gttctgtttg ccatcctgaa gatgccatca accactggga gacaaaaggc cttttccacc 720  
 tgtgccgctc acctcacatc tgtgacccta ttctatggca cagccagtat gacttattta 780  
 caacccaaat ctggctactc accggaaacc aagaaagtga tgtcattgtc ttactcattt 840  
 ctgacaccac tgctgaatct gcttatctac agtttgcgaa atagttagat gaagagggtc 900  
 ttgatgaaat tatggcgaag gcgagtgggt ttacacacaa tc 942

<210> 938  
 <211> 993  
 <212> DNA  
 <213> Unknown (H38g788 nucleotide)

<220>  
 <223> Synthetic construct

<400> 938  
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tttgggctct	tctccctgtt	ctatgtcttc	accctgctgg	ggaatgggac	catcctgggg	120
ctcatctcac	tggactccag	actccacacc	cccatgtact	tcttcctctc	acacctggcc	180
gtcgtcaaca	tcgcctatgc	ctgcaacaca	gtgccccaga	tgctgggtgaa	cctcctgcat	240
ccagccaagc	ccatctcctt	tgttggtctg	atgacataga	cctttctctt	tttgagtttt	300
gcacatactg	aatgcctcct	gttggtgctg	atgtcctacg	atcggtacgt	ggccatctgc	360
cacctctctc	gatatttcat	catcatgacc	tggaaagtct	gcatactctt	ggccatcaact	420
tcttggaacat	gtggctccct	cctggctatg	gtccatgtga	gcctcactct	aagactgccc	480
ttttgtgggc	ctcgtgaaat	caaccacttc	ttctgtgaaa	tctgtctgtg	cctcaggctg	540
gctgtgctg	atacctggct	caaccagggtg	gtcatctttg	cagcctgcat	gttcactcctg	600
gtggggaccac	tctgcctggg	gctgggtctcc	tactcacaca	tcttgggcgc	catcctgagg	660
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ctgattttaca	acctgaggaa	tgtagagggtc	aagggtgccc	tgaggagagc	actgtgcaag	900
gaaagtcatt	cctaagagggt	gtgacatttg	aactgccagc	ctcagttgtc	acgtgggactc	960
ttgatgcccc	attattgcct	caatccagaa	aag			993

&lt;210&gt; 939

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g789 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 939

atggggggaca	atataacatc	catcacagag	ttcctcctac	tgggatttcc	cgttggccca	60
aggattcaga	tgctcctctt	tgggctcttc	tccctgttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgacagcccc	catgtacttc	180
ttcctctcac	acctggcggt	cgctgacatc	gcctacgcct	gcaacacggg	gccccggatg	240
ctgggtgaacc	tctgtcatcc	agccaagccc	atctcctttg	cgggccgcat	gatgcagacc	300
tttctgtttt	ccacttttgc	tgctcacagaa	tgtctcctcc	tgggtggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttgccca	tcatgacctg	gagagtctgc	420
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ttggctgttc	tcaaacttgc	ctgtgcagat	acccacatca	atgagaacat	ggtcttggcc	600
ggagcaattt	ctgggctggg	gggacccttg	tccacaattg	tagtttcata	tatgtgcata	660
ctctgtgcta	tcttccagat	ccaatcaagg	gaagttcaga	ggaaagcctt	ctgcacctgc	720
ttctcccacc	tctgtgtgat	tggactcttt	tatggcacag	ccattatcat	gtatgttggg	780
cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	cgctgtttca	cagcctcttt	840
aatcccatgc	tcaatccctt	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtttta				930

&lt;210&gt; 940

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g790 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 940

atgaaaagac	aaaatcaaag	ctgtgtgggt	gaattcatcc	tcttgggctt	ttctaacttt	60
cctgagctcc	agggtgcagct	ctttgggggt	ttcctagtta	tttatgtggg	gaccctgatg	120
ggaaatgcca	tcattacagt	catcatctcc	ttaaaccaga	gcctccacgt	tcccatgtac	180
ctgttctctc	tgaacctatc	tgtggtggag	gtgagtttca	gtgcagtcac	tacgcctgaa	240
atgctgggtg	tgctctctac	tgagaaaact	atgatttctt	ttgtgggctg	ttttgcacag	300
atgtatttca	tccttctttt	tgggtgggact	gaatgttttc	tcttggggagc	gatggcttat	360
gaccgatttg	ctgcaatttg	ccatcctctg	aactaccag	tgattatgaa	cagaggggtt	420
tttatgaaat	ctgtaataat	ctcatggatc	tcagggaatc	tgggtggctac	tgtgcagacc	480
acttgggtat	ttagtttttc	attttgtggc	cccaatgaaa	ttaatcatct	cttctgtgag	540

actcccccg	tactagagct	tgtgtgtgca	gacaccttct	tatttgaaat	ctatgccttc	600
acaggcacca	ttttgattgt	tatggttcct	ttcttgttga	tcctcttgte	ttacattcga	660
gttctgtttg	ccatcctgaa	gatgccatca	actactggga	gacaaaaggc	cttttccacc	720
tgtgcctctc	acctcacatc	tgtgacctg	ttctatggca	cagccaatat	gacttattta	780
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cttacccttc	tgctcaatcc	gctcatctat	agcttacgaa	acagtgagat	gaagaggact	900
ttgataaaac	tatggcgaag	aaaagtgatt	ttacacacat	tc		942

&lt;210&gt; 941

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g791 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 941

atgagtgc	acacctccat	ggtgactgag	tttcttcttc	tcggcttctc	ccacctggcc	60
gacctccagg	gcttgtctct	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatttctctca	ttgtgggtgct	ggctctccact	gatgctgccc	tccagtcctc	tatgtacttc	180
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ttcttcttcc	tcttcttttg	cgccacggag	tgctgcctcc	tggcagccat	ggcctatgac	360
cgctatgcag	ccatctgtga	acccctccgc	taccactgc	tgctgagcca	ccgggtgtgt	420
ctacagctag	ctgggtcggc	gtgggcctgt	gggtgctgg	tggggctggg	ccacaccct	480
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cagcctgtcc	tgcagctggt	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
gcaacagccc	tcctcatcct	ctgccccttt	ggcctcatcc	tgggctccta	cgggcgtatc	660
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tcttcccacc	tgategtggt	ctccctcttc	tatggcaccg	cactctttat	ctatattegc	780
cctaaggcca	gctaagatcc	ggccactgac	cctctggtgt	ccctcttcta	tgctgtggtc	840
acccccatcc	tcaaccccat	catctacagc	ctgcggaaca	cagagggtcaa	agctgcctta	900
aagagaacca	tccagaaaac	ggtgcctatg	gagatt			936

&lt;210&gt; 942

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g792 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 942

atgtacctgg	tcactgtgct	cgggaaacctg	ctcatcatcc	tggccgcaat	ctcagactcc	60
tgcttccaca	ccccatgta	cttctttctc	tccaacctgt	ccttcgtaga	tatctgtttt	120
gcctccacca	tgggtccaaa	gatgttggtg	aacatccaga	cacagagcaa	agtcattacc	180
tatgcagggt	gcatcaccca	gatgtgcttt	tttgtactct	ttatagtgtt	ggacagctta	240
ctcctgaccg	tgatggccta	tgaccagttt	gtggccatct	gtcaccctct	gcactacacg	300
gtcatcatga	gccctcagct	ctgtggactg	ctgggtcttg	tgctcctggat	catgagtgtc	360
ctaaactcca	tgttacaaa	cttagtgaca	ttgcagttgt	ccttctgcac	agacttgga	420
atccctcact	ttttctgtga	acttaatgag	atgatccacc	ttgcctgttc	tgacaccttt	480
tggaacaaca	tgggtgatga	ttttgcagct	gtgctgctgg	acgggtggte	tctcgttggg	540
atccttttatt	cttactgtag	gatagtttcc	tccatacgtg	caatctcgtc	aactcagggg	600
aagtacaagg	cactttccac	ctgtgcatct	cacctctcag	ttgtctccat	attttatggt	660
acggggctag	gggtgtacct	tagctctact	atgacccaaa	acttacactc	aactgctgtc	720
gcctcggtga	tgtacactgt	ggtcaccccc	atgctcaacc	ccttcattta	cagtctgagg	780
aataaagaca	taaagggggc	tctgacacaa	ttcttcagag	ggaaacaa		828

&lt;210&gt; 943

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g793 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 943

tcaattacct	gggaaaatca	ctcagtgttg	atggaatttg	tgttcctggc	ctatccctcc	60
tgcccagaac	tgcatattct	gtccttccct	ggggtcagcc	tggtttatgg	tttgatcatc	120
actgggaaca	ttctcattgt	ggtgtccatt	cacacagaaa	cctgtctatg	cacatccatg	180
tactatttcc	tgggcagcct	ttctgggatt	gaaatatgct	acactgcagt	ggtgggtgcc	240
catatcctgg	ccaacaccct	acagtcagag	aagacatcac	tctcctgggc	tgtgccaccc	300
agatggcttt	cttcattgca	ctgggcagtg	ctgattgctt	cctcttggct	gccatggcct	360
atgaccgcta	tgtggccatt	tgccaccctg	tgcagtaccc	tctcctcatg	acattgactc	420
tttgtgtcca	cttgggttgtg	gcatacgtca	tcagtgggtct	gttcctgtcc	ttacaactgg	480
tggccttcat	cttctctctg	ccattctgcc	aggctcaggg	cattgagcac	ttctttttgtg	540
atgtgccacc	agtcattgcat	gttgtttgtg	ctcagagtca	cattcatgag	cagtcagtcg	600
tgggtggcagc	catactagcc	attgctgtgc	ctttcttcct	catcaccacc	tcctacacct	660
tcatagtggc	tgtctctgtc	aagatccact	cggctgctgg	ccgccaccgg	gccttctcca	720
cctgctcttc	ccacctcaact	gtgggtgctgc	tgcagtatgg	ctgctgtgcc	ttcatgtacc	780
tgtgccccag	ctccagctac	aaccccaagc	aagatcggtt	catctcactg	gtgtacacat	840
tgggaacccc	actgctcaac	ccacttatct	atgcctgag	gaacagtgag	atgaaagggg	900
ccgtagggag	agttcttacc	aggaactgcc	tttcccagaa	cagctaggaa		950

&lt;210&gt; 944

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g794 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 944

atggaaccag	agaatgacac	agggatttca	gaatttgctc	ttctgggact	ttctgaggaa	60
ccagaattgc	agcccttccct	ctttgggctg	tttctgtcca	tgtacctggt	cactgtgctc	120
gggaatctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttccctct	ccaacctgtc	ctttgcagac	atctgtttca	tctccactac	aatcccaaag	240
atgtctatta	acatccagac	acagagcaga	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	ttgtactttt	tggagggtta	gacagcttac	tcctggctgt	gatggcctat	360
gatcggtttg	tggccatctg	tcatectctg	cactacacag	tcatacatgaa	ccctcggtc	420
tgtggactcc	tgggtctggc	atcctggatg	attgctgccc	tgaattcctt	gtcacaagc	480
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cttaatcagg	tcataccact	tgcctgttct	gacaccttct	ttaatgacat	ggggatgtat	600
tttgcagcag	ggctgctggc	tgggtggccc	cttgtgggga	tcctttgtct	ttactctaag	660
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gccaccccca	tgtgaaccc	ctttatctac	agtctgagga	ataaagacat	aaagagggct	900
ctgaaaatgt	ccttcagagg	aaagcaa				927

&lt;210&gt; 945

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g795 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 945

atggagaata	atacagaggt	gagtgaattc	atcctgcttg	gtctaaccac	tgccccagaa	60
ctacagggtc	ccctctttat	catgtttacc	ctcatctacc	tcatactctc	gactgggaac	120
ctggggatga	tcataattaat	cctgctggac	tctcatctcc	acactcccat	gtactttttt	180

ctcagtaacc	tgtctcttgc	aggcattggg	tactcctcag	ctgtcactcc	aaagggtttta	240
actggggtgc	ttatagaaga	caaagccatc	tcctacagtg	cctgtgctgc	tcagatgttc	300
ttttgtgcag	tctttgccac	tgtggaaaat	tacctcttgt	cctcaatggc	ctatgaccgc	360
tacgcagcag	tgtgtaaccc	cctacattat	accaccacca	tgacaacacg	tgtgtgtgct	420
tgtctggcta	taggctgtta	tgtcattggg	tttctgaatg	cttctatcca	aattggagat	480
acatttcgcc	tctctttctg	catgtccaat	gtgattcatc	actttttctg	tgacaaacca	540
gcagtcatta	ctctgacctg	ctctgagaaa	cacattagtg	agttgattct	tgttcttata	600
tcaagtttta	atgtcttttt	tgcacttctt	gttaccttga	tttccatctt	gttcatattg	660
atcaccattc	ttaagaggca	cacaggtaag	ggataccaga	agcctttatc	tacctgtggg	720
tctcacctca	ttgccatttt	cttattttat	ataactgtca	tcacatgta	catagacca	780
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cccattgctc	gtcctatagt	ctataccctg	aggaacaaag	acgtgaagaa	tgcattcatg	900
aagggtgttg	agaaggcaaa	atattctcta	gattcagtct	tt		942

&lt;210&gt; 946

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g796 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 946

atgtaaaata	actcaaagtt	tactgatttc	atcctggtag	gtctaaccac	tgccacagaa	60
cttcagatcc	ccctctttat	cttgttcata	ctcatccacc	tcctcattct	gactaggaac	120
ctggagatca	tactgttgat	cctgctggac	tcttgtctcc	aattcccatg	tactttttcc	180
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tgtcatctcg	gtcataggct	cctatgtctg	tggtcttcta	aatgcctccc	tcgcattggg	480
ggacatatct	agtctctctt	tctgtaagtc	caatcttgtc	catcaccttt	tctgtgatgt	540
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gcctagctcc	agccattcca	tggacacaga	tgaaatggca	tccttgttct	atgctgtgtt	840
catctccatg	ctgaaccttg	tgttctacag	cctgaggagc	aaagaagtca	agaatgcatt	900
caaaaaggcg	gttgagaagg	caaaattttt	cttagaactg	tgattt		946

&lt;210&gt; 947

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g797 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 947

atggacaaca	gcaactggac	cagtgtgtcc	cattttgttc	tcttgggcat	ttccaccac	60
ccagaagagc	aaatcccact	cttcccttgt	ttctcactca	tgtaacgaat	caatatttct	120
ggcaacttgg	ccatcatcac	actgattctc	tctgtccac	gcctccacat	ccccatgtac	180
atcttcctca	gtaacttggc	cttgacagac	atctgtctca	cctccaccac	ggtccccaag	240
atgctgcaga	ttattttctc	ccctacaaaag	gtaatttctt	acacaggctg	tttagcccaa	300
acttatttct	tcatttgcct	cgccgtcatg	gaaaacttca	tcctggctgt	gatggcctat	360
gacagggtaca	ttgccatctg	ccaccctttc	cactacacta	tgatcctgac	tagaatgctg	420
tgtgtgaaga	tggtggatcat	gtgccatgct	ctctcccacc	ttcatgccat	gctgcatacc	480
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gtgactccca	tgctgaaccc	cttcactctac	agcctgagga	atggggatgt	caagggaggc	900
ttcatgaaat	ggatgagcag	aatgcagact	ttttcttta	ga		942

&lt;210&gt; 948

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g798 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 948

atgggtaacc	aaagctcccc	catgggcttc	ctccttctgg	gcttctctga	acaccagca	60
ctggaaagga	ctctctttgt	ggttggtctc	acttcctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tctgtctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
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gtcaacctct	ggggcccaaa	gaagaccatc	agcttcctgg	gatgctctgt	ccagctcttc	300
atcttcctgt	ccctggggac	cactgagtgc	atcctcctga	cagtgatggc	ctttgaccga	360
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agtgtcatct	tctgtggtgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
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aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttcactta	acctctctgt	atacacctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

&lt;210&gt; 949

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g799 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 949

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gatccagaag	tgacagccgt	cctcgtcttg	ctgtccctgt	ccctgtccat	gtatatggtc	120
acggtgctga	ggaacctgct	cagcactctg	gctgtcagct	ctgactcccc	gctccacacc	180
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gttcccaaga	tgattgtgaa	catgcagtcg	catagcagag	tcattctctta	tgagggtctg	300
ctgacacgga	tgtctttctt	tgtccttttt	gcattgtatg	aagacatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
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tactataaaa	ttgtccctct	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaggc	720
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tatgtctgtg	tcacccccat	gctgaacctt	ttcatctaca	gcctaggaaa	gagggatata	900
caaagtgtcc	tgcgagggct	gtgcagcaga	acagtcgaat	ctcatgatat	gttccatcct	960
ttttcttgtg	t					971

&lt;210&gt; 950

&lt;211&gt; 474

&lt;212&gt; DNA

<213> Unknown (H38g800 nucleotide)

<220>

<223> Synthetic construct

<400> 950

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ggaaacctgc	tcatactcct	ggccatctgc	tctgggtccc	acctccacac	ccccatgtac	180
ttcttctctc	ctaacctgtc	ctttgtagac	atctgtgtta	cctccaccac	agtcctcaaag	240
acactgtcaa	acatccggac	acagagtaaa	gtcatcacct	atgcagggtg	catcacccag	300
atgtactttt	ttgtactctt	tatagtgttg	gacagcttac	tcttgaccgt	gatggcctat	360
gaccagtttg	tggccatctg	tcacccccctg	cactacacgg	tcacgtgaa	ccctcggtctc	420
tgtggactgc	tggttctggc	gtcctggatc	atgagtggcc	tgaattcctt	gata	474

<210> 951

<211> 954

<212> DNA

<213> Unknown (H38g801 nucleotide)

<220>

<223> Synthetic construct

<400> 951

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agagctaaca	tctcctacac	tctcctcttc	ttcctgttcc	tggctattta	cctgaccacc	120
atactgggga	atgtgacact	ggtgctgctc	atctcctggg	actccagact	gcactcacc	180
atgtattatc	tgcttcgtgg	cctctctgtg	atagacatgg	ggctatccac	agttacactg	240
ccccagttgc	tggcccattt	ggtctctcat	tacccaacca	ttcctgctgc	ccgctgcttg	300
gctcagttct	ttttcttcta	tgcatttggg	gttacagata	cacttgtcat	tgctgtcatg	360
gctctggatc	gctatgtggc	catctgtgac	cccctgcact	atgctttggg	aatgaatcac	420
caacgggtgtg	cctgcttact	agccttgagc	tgggtgggtg	ccatactgca	caccatgttg	480
cgtgtgggac	tcgtcctgcc	tctttgctgg	actggggatg	ctggggggcaa	cgtaaacctt	540
cctcacttct	tttgtgacca	ccggccactt	ctgcgagcct	cttggtctga	catacattct	600
aatgagctgg	ccatattctt	tgagggtggc	ttccttatgc	tgggcccctg	tgccctcatt	660
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cgccgagcag	tctccacctg	tggatccccc	ctcaccatgg	ttgggttctc	ctacgggcacc	780
atcatttgtg	tctacttcca	gcctcccttc	cagaactctc	agtatcagga	catggtggct	840
tcagtaatgt	atactgccat	tacacctttg	gccaaacctat	ttgtgtatag	cctccacaat	900
aaggatgtca	agggtgcact	ctgcaggctg	cttgaatggg	tgaaggtaga	cccc	954

<210> 952

<211> 921

<212> DNA

<213> Unknown (H38g802 nucleotide)

<220>

<223> Synthetic construct

<400> 952

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ctgcagcctt	ttctcttcgt	ggttttcttc	accatctact	tcatacagtg	gactgggaat	120
ggagccgttc	tgatgattgt	catctccgat	cctagactcc	attcccttat	gtatttcttc	180
ctgggaaacc	tgtcctacct	ggatatctgt	tactctacgg	tgacactgcc	aaaaatgctg	240
cagaactttc	tctctacaca	caaagcaatt	tctttcttgg	gatgcataag	ccagcttcat	300
ttcttccact	tcttgggcag	cacggagtcc	atgttgttcg	ccgtgatggc	atttgacctc	360
tctgtggcta	tctgcaagcc	acttcgctac	actgtcatca	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	ggtcatttgg	tttttccatg	ccctgctgca	ctccgtaatg	480
acttctcgct	tgaacttctg	tggttccaac	cgtatccatc	attttctctg	tgatattaag	540
ccattgctaa	agctggcctg	tgggaacact	gagcttaatc	agtggctact	cagtactgtc	600
acggggacaa	ttgccatggg	ccccttcttt	ctgacacttc	tctcctattt	ctacattatc	660

acttatctct	tcttcaagac	ccgttcttgt	agcatgctct	gtaaagcact	gtccacttgt	720
gcctcccaact	tcattgtagt	tattcttttc	tatgcacctg	ttcttttcac	ctatatccat	780
cctgcgttag	agagcttcat	ggaccaggac	cggattgttg	ccatcatgta	cactgtggtc	840
actcctgtac	taaaccctact	gatctatact	ttgaggaaca	aggaagtga	gggggccttg	900
ggtagagtga	tcagaaggct	t				921

&lt;210&gt; 953

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g803 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 953

cagccacgga	atctcacaga	tgtctgagaa	ttcctcctca	tgggactctc	agaggatcca	60
gaactgcagc	ccgtcctcgc	tgggctgtcc	ctgtccatgt	atctggtcac	gggtgctgagg	120
aacctgctca	gcacccctggc	tgtcagctct	gactccacc	tccacacccc	catgtacttc	180
ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cggccacggg	tcccaagata	240
attgtggaca	tgcagtcgca	tagcagagtc	atctcttatg	tgggctgcct	gacacggatg	300
tcttttttgg	tcctttttgc	atgtatagaa	gacatgcttc	tgactgtgat	ggcctatgac	360
tgctttgtag	ccatctgtcg	ccctctacac	taccagtc	tcgtgaatgc	tcacctccgt	420
gtcttcttag	ttttgggtgc	cttttccctt	agcctgttgg	attcccagct	gcacagttag	480
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tctcaacttc	tcaagcttgc	ctgttctgac	agcatcatca	atagcatatt	catatatattc	600
gatagtacta	tgtttggttt	tcttcccatt	tcagggatcc	ttttgtctta	ctgtaaaatt	660
gttccctcca	ttctaaggat	ttcaacatca	gatgggaaat	ataaagcctt	ctccacctgt	720
ggctctcacc	tggcacttgt	ttgcttattt	tatggagcag	gcattggcgt	gtacctgact	780
tcagctgtgt	caccaccccc	caggaatggt	gtggtggtgt	cagtgatgta	cactgtggtc	840
accccatgc	tgaacccttt	catctacagc	ctgagaaaca	gggacattca	aagcaccttg	900
cggaggctgc	tcagcagaac	agtcgaatct	catgatctgt	tccatccttt	ttcttgtgt	959

&lt;210&gt; 954

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g804 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (984)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 954

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
ccagatctcc	agtccctct	gttcttccctg	tttctagtaa	tctatgtggt	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttccctct	ttaacttgtc	cttcatagat	ctctgttatt	cttctgtgtt	tatacccaaa	240
atgctaata	actttatttc	agagaagaat	attatgtcct	tcaaggggtg	catgacccaa	300
ctttccctttt	ncgtattttt	ttgggtcattt	ctgaagggtta	tgtgctgacg	tcaatggcgt	360
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aacctatctt	ctgtgtgggtc	catggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtgggttccc	tggtgaaccc	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960



agtcacaaga cagggatatt ctgt

984

&lt;210&gt; 955

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g805 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 955

atgggaagaa	ataacctaac	aagaccctct	gaattcatcc	tccttggact	ctcctctcga	60
cctgaggatc	agaagccgct	ctttgctgtg	ttcctcccca	tctaccttat	cacagtata	120
ggaaacctgc	ttatcatcct	ggccatccgc	tcagacactc	gtctccagac	gccccgtac	180
ttctttctaa	gcatacctgc	ttttgttgac	atttgctatg	tgacagtcat	tatccctaag	240
atgctggtga	acttcttate	agagacaaaag	accatctctt	acagtgaagt	tctgacccag	300
atgtactttt	tcttagcctt	tggaacacaca	gacagttacc	tgctagcagc	catggccatt	360
gaccgctatg	tggccatatg	taatcccttc	cactacatca	ccattatgag	tcacagatgc	420
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cagccctgt	ccaactatac	tgtcaaggat	caaatagcaa	caattatcta	caccgtactg	840
actcctatgc	taaateccatt	tatctatagt	ctgaggaaca	aagacatgaa	gcagggtttg	900
gcaaagttga	tgcacaggat	gaaatgtcag				930

&lt;210&gt; 956

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g806 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 956

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggtctctat	60
gacatccctg	aactgcattt	cttggttttt	attgtattca	ctgctgtcta	tgtcttcac	120
atcatagggg	atatgctgat	tattgtagca	gtgggttagct	cccagaggct	ccacaaaccc	180
atgtatattt	tcttggcgaa	tctgtccttc	ctggatatcc	tctacacctc	cgcagtgatg	240
ccaaaaatgc	tggagggtct	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgtaccaca	ctccactacc	cactcctgat	ggggcccaga	420
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ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgct	gagagttcct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgctcct	cccacctagc	tgtagtgacc	acattctatg	gaacgctcat	gatcttttat	780
gttgaccctc	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcacc	ctctcttcaa	tctgtgatc	tatacatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaaaa	actgaaacac	ttgat		945

&lt;210&gt; 957

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g807 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 957

cactggaaaa	ttttaagaag	aaacagcaag	atgatacatg	aaattatata	gaccttatgc	60
caaateccttt	actcagagga	caaaacttgt	tacatacaga	tacaaagctt	gttttgtact	120
gacttgga	tcccaaactt	tttctgtgaa	cttaattagg	tggtccacct	tgctgttct	180
gacacctttc	tcaaagacat	agtggaggtat	tgtacaacta	tgctgctgag	tggtgggtccc	240
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agctcagggg	aagcataaag	catttcccaac	ctgctgtgtct	cacctctcaa	atatgtcctt	360
attttattgt	aggagcacag	gattgtacct	tagttttgct	gctaccaca	actcatgctc	420
taatgcaact	gcctcagtga	ggcacactgt	ggtaaacc	ttactaaacg	tttcatctt	480
aaagtcaagt	aataaagaca	taaaatgagc	tctgaaagta	ttcttcagag	gaaagcaatg	540
gaagcatcat	ttttcaaaaa	gtgca				565

&lt;210&gt; 958

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g808 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 958

atggaaaaaa	gaaatctaac	agttgtcagg	gaattcgtcc	ttctgggact	tcctagctca	60
gcagagcagc	agcacctcct	gtctgtgctc	tttctctgta	tgtatttagc	caccaccttg	120
gggaacatgc	tcattcattgc	gacgattggc	tttgactctc	acctccattc	ccctatgtac	180
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ctcttcttct	tcgtttcttt	tgtgaatatg	gacagcctcc	ttctgtgtgt	gatggcgtat	360
gatagatatg	tggcgatttg	ccacccctta	cattacaccg	ccagaatgaa	cctgtgcctt	420
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gtggctccga	tgctgaatcc	tttcatctat	accctaagga	acagggatat	gaagagggga	900
cttcagaaaa	tgcttctcaa	gtgcacagtc	tttcagcag			939

&lt;210&gt; 959

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g809 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 959

atggatggag	gcaaccagag	tgaaggttca	gagttccttc	tcctggggat	gtcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggt	cacggtggtg	120
ggaaatgtgc	tcattcatcct	ggccatcagc	tctgattccc	gcctgcacac	ccccgtgtac	180
ttcttcctgg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaa	240
atgctgggtga	acctccagtc	ccataacaaa	gccatctcct	atgcagggtg	tctgacgcag	300
ctctacttcc	tgggtctcctt	gggtggccctg	gacaacctca	tcctggctgt	gatggcatat	360
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tgtatcttac	tcctttcctt	gtgttgggtc	ctatccgtcc	tctatggcct	catacacacc	480
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gccacaggct	gcttcatctt	cctcatctcc	tttggattcg	tgatcatttc	ctatgtgctg	660
attatcagag	ccatccctcag	aataccctca	gtctctaaga	aatacaaaagc	cttctccacc	720
tgtgcctccc	atttgggtgc	agtctccctc	ttctatggga	cactttgtat	ggtatacctc	780

aagccccctcc atacctactc tgtgaaggac tcagtagcca cagtgatgta tgctgtggtg 840  
 acacccatga tgaatccctt catctacagc ctgaggaaca aggacatgca tggggctctg 900  
 ggaagactcc tagataaaca ctttaagagg ctgaca 936

<210> 960

<211> 951

<212> DNA

<213> Unknown (H38g810 nucleotide)

<220>

<223> Synthetic construct

<400> 960

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 tctgaagacc agaggccact ctttgccctc tttcttatca tatacctggg cactttgatg 120  
 ggaaatctgc tcatcatctt ggctatccac tctgatccct gacttcaaaa ccctatgtat 180  
 tttttcctaa gcatcttgct ctttgctgat atttgctaca caacagtcac agtcccaaaag 240  
 atgctcgatga acttcttata agagaaaaag accatttcct atgctgaatg tctggcacag 300  
 atgtatttct tcctgggttt tggaacata gatagttatc tcctggcggc tatggccatc 360  
 aaccgctgtg tagccatttg taacccattc cattatgtca ctgttatgaa ccgcagatgc 420  
 tgtgtgttgc tactagcatt ccccatcact ttctcctatt tccactctct cctacatgct 480  
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 gtcaaccctg tgctgaaact gtcctgctcc tccacctttg tcaatgaaat tgtggccatg 600  
 acagaagggg tggcctctgt gatggctcca tttgtctgta tcatcatctc ttatctaaga 660  
 attctcatcg ctgttctcaa gattccctca gcagctggaa aacacaaagc cttctccacc 720  
 tgcagctccc atctcactgt ggtgattctg ttttatggga gtattagcta tgtctatttg 780  
 cagcctttgt ccagctatac tgtcaaggac cgaatagcaa caatcaacta cactgtgttg 840  
 acatcagtggt tgaacccatt tatctacagt ttaagaaaca aagacatgaa acggggctta 900  
 cagaaattga taacaagat taagtctcaa atgagtaggt tctctacaaa g 951

<210> 961

<211> 926

<212> DNA

<213> Unknown (H38g811 nucleotide)

<220>

<223> Synthetic construct

<400> 961

atgctgaata caacctcagt cactgaattt ctcttttttg gagtgacaga cattcaagaa 60  
 ctgcagcctt ttctcttcgt tgttttcctt accatctact tcatcagtggt ggctgggaat 120  
 ggagccattc tgatgattgt catctctgat cctagactcc attcccctat gtatttcttc 180  
 ctgggaaacc tgcctgcct ggacatctgc tactccagcg taacactgcc aaaaatgctg 240  
 cagaacttcc tctctgcaca caaagcaatt tctttcttgg gatgcataag ccaactccat 300  
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 cagatggcca tcacaatctg gatgattggt tttttccatg ccctgctgca ctccctaattg 480  
 acctctcgct tgaacttctg tggttctaac cgtatctatc acttcttctg tgatgtgaag 540  
 ccattgctaa agctgagctt aatcagtggc tgctcagtac tgtcacaggg acaatcgcca 600  
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 agactcattc ttttagcatg ctccgcaaaag cactgtccac ttgtgcctcc cacttcatgg 720  
 tagttattct tttgatgca cctgttctct tcacctatat tcatcatgcc tcagggaacct 780  
 ccattggacca ggaccggatc actgccatca tgtatactgt ggtcactcca gtactaaacc 840  
 cactgatcta cactttgagg aacaaggaag tgaaaggggc ctttaataga gcaatgaaaa 900  
 ggtggctttg gcctaaagaa atcttg 926

<210> 962

<211> 983

<212> DNA

<213> Unknown (H38g812 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 962

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tccttggaaa	tgcagttttt	cctttttctc	ttcttctctt	tattctatgt	gggaattatc		120
ctgggaaacc	tcttcattgt	gttcacagtg	atctttgatc	ctcacttaca	ctcccccatg		180
tatattctgc	tggccaacct	atcgctcatt	gacttgagcc	tttcatctac	cacagttcct		240
aggttgatct	acgatctttt	tactgattgt	aaagttattt	ccttccataa	ttgtatgata		300
caaaagttct	ttatccatgt	tacgggagga	gttgaaatgg	tgctgctgat	agtcatggaa		360
tatgataggt	acactgcat	ctgcaagcct	ctccactatc	caactattat	gaatcccaaa		420
atgtgcatgt	ttttggtagc	agcagcttgg	gtcattgggg	tgattcatgc	tatgtctcag		480
tttgtttttg	tcataaatta	accttctgtg	gccctaataa	tgtggggagc	ttttattgtg		540
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ctgccaacag	tggattcata	tcgatgggca	ccttcttttt	cttaattgta	tcatacattt		660
ttattctggt	cactgtccaa	cgacattcct	caaagtattt	atccaaagca	ttcttctactt		720
cgtaggctca	catcacgcta	gtggttttgt	tttttgcctc	atgcatgttt	ctctacgtgt		780
ggcctttccc	tactaagtca	ttggataaat	tttttggcat	catgaacttt	gttgtcaccc		840
ctgtcttaaa	tcctgccatc	tatactttta	ggaacaaaga	tatgaagttt	gcaatgagaa		900
ggctgaatca	acataatttta	aattctatgg	agacgacata	acacatttgg	ttgatgagag		960
cacaggataa	atgccatgga	cca					983

&lt;210&gt; 963

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g813 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 963

atgtggatca	acaatcaaag	ctcgctagat	gattttatcc	tattgggatt	ttctgaccgt	60
ccctggctag	agacacccct	ctgtaatctt	tctgggtggc	tacatctttt	ccctatttgg	120
aaatatctcc	attatcctag	tttcccatct	ggatccccag	cttgacagtc	ccatgtactt	180
ttttgtctct	aatctatcct	ttctggacct	ctgctatacc	accagcactg	tcccacagat	240
gctgggtcaac	ctccgggggac	cagaaaagac	cattagctat	gggggttgtg	ttgcccact	300
ctatatattt	ttggccctgg	gttctactga	atgcatactt	ctagccatca	tggcctttga	360
ccgttacgct	gcatatgca	agccccctca	ctaccagtc	atcatgaacc	atagacgctg	420
tatccacatg	gctgctggca	cttggatcag	tggtcttgtc	aactcccttg	tccagtccac	480
tctcacagtg	gtggccccaa	gatgtggaca	gagggtgttg	gaccatttct	tctgtgaagt	540
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actaggcgct	ttgcttctcc	tgatgccact	caccctcatc	ctgggcactt	atgtgttcat	660
tgctcaggca	gtaatgagaa	tctgctctgc	tgaaagtgcg	tggaaggctt	tcaatacctg	720
tgctcaccat	ttgctgggtg	tctccctctt	ctacttcaca	gccatcagta	tgtatgtcca	780
gcctccctct	agctattctc	atgaccgggg	gaagatc			817

&lt;210&gt; 964

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g814 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 964

atgaatgtct	ctgagccaaa	ttccagcttt	gcttttgtaa	atgaatttat	actccaaggt	60
ttctcttgtg	agtggacaat	tcagatcttc	ctcttctcac	tctttactac	aacatatgca	120
ctgactataa	caggggaatg	agccattgct	tttgtcctgt	ggtgtgaccg	gcgacttcac	180
actccccagt	acatgttctt	gggaaatttc	tcctttttag	agatatggta	tgtctcttct	240
acagttccca	agatgttggg	caacttcctt	tcagagaaaa	aaaacatctc	ctttgctgga	300
tgttttctcc	agttttattt	cttcttctct	ttgggtacat	cagaatgctt	gcttttgact	360

gtgatggcct	ttgatcagta	ccttgctatc	tgccgtccct	tgtcttatcc	taatatcatg	420
actgggcac	tctatgccaa	actggtcata	ctgtgctggg	tttgtggatt	tctgtgggtc	480
ctgatcccca	ttgtttctcat	ctctcagatg	cccttctgtg	gccccaaacat	tattgacccat	540
gttgtgtgtg	acccagggcc	acgatttgca	ttggattgtg	tttctgcccc	aagaatccaa	600
ctgttttct	acactcctaag	ctcattagtt	atttttggta	acttcctctt	tattatttga	660
tcctatactc	ttgtcctgaa	agctatgttg	ggatgcctt	caagcactgg	gagacataag	720
gccttctcta	cctgtgggtc	tcatttggct	gtggtatcac	tgtgctatag	ctctcttatg	780
gtcatgtatg	tgagcccagg	actcggacat	tctacagggg	tgcagaaaat	tgaaactttg	840
ttctatgcta	tggtgacccc	actcttcaat	cccccttatc	atagcctcca	gaataaggag	900
ataaaggcag	ccctgaggaa	agttctgggg	agttccaaca	taatc		945

&lt;210&gt; 965

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g815 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 965

atggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttecta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgac	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcactctctt	caagggtctg	cttggtcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtgat	cctcatagcc	atgggctatg	acagatatat	agcaatatgc	360
aaaccactaa	actacactac	aattatgtgt	ggcaacgc	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgtctact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgcccttttag	ataagtctgt	caaagctctg	tccactttga	ctgtctacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgtctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 966

&lt;211&gt; 953

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g816 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 966

atgacattac	ccagcgatga	ctccactgtc	ccagtctctg	aattcctcct	catctgcttc	60
cccaactttc	agagttggca	gcacttgctg	tccttgcccc	tcagcctcat	ttcctcctgg	120
ccatggggac	caacacccac	cccccccatc	accatccacc	tggaggcctc	tctgcacctg	180
cccctgtact	acctgcccag	cctcctctcc	ctgctggaca	tcgtgctctg	cctcaccgtc	240
atccccaagg	tcctggccat	cttctggttt	gatcttaggt	cgatcggctt	ccctgcctgc	300
ttccttcaga	tgttcacat	gaacagtttc	ctccccattg	agtcctgcac	attcatggtc	360
aaggactatg	atcattatgt	ggccatctgc	caccactgc	agtacctgtc	catcatcact	420
catcaatttg	tggccaaagc	tagtgtcttc	atttgtgtgc	agaatgcttt	gctgctttca	480
cctgttctca	ttctctctgc	ccagctccat	tactgttagga	aaaatgtgat	tgagaactgc	540
atctgtgcca	acctgtctgt	gtccaggctc	tcctgtgata	atttcaccct	taacagactc	600
taccaatttg	tggctgggtg	gaccttcctg	ggctcggatt	tcctcctcat	cttcctctcc	660
tacaccttca	ttctaagagc	tgtgcttaga	ttcaagggtg	aggggggtgg	agtgaaggcc	720
ctgagcacat	gtggctccca	ctttatcctc	atcctcttct	tcagcacctg	ctggttgtgg	780
gtttgacaaa	tgtggccaga	aagaaggctc	ccatggacat	cctgatcctg	tttaatgtcc	840
ttcatccctt	tagtctcct	gcattaaacc	ctatcatatg	tggatttcaa	actaaagagt	900

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg

953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

aaacacaatc	acacggcagt	gaccaaggtg	actgaattta	ttctcatggg	gattacagac	60
aaccctgggc	tgcaggctcc	actgtttgga	ctcttcctca	tcatatatct	ggtcacagt	120
ataggcaatc	tgggcatggt	tatctttgac	ctactttgga	ctccaagcta	cacaccccca	180
tgtacttttt	ccttaaacad	ttggcaatca	ctgatctttg	gttactccac	tgtcattggg	240
cccaaagat	gtttagtga	acctcatatg	tgcacaaaga	acacaatttc	ttttacaatt	300
ggtagtccaa	tcacagagca	cgctttgaga	ggaacatcat	ctctcaccgc	ggcattctat	360
cagcaacgaa	caatgagccc	tacaaaccca	tcactaaaca	acttctgaac	ccgatcatca	420
tgccagagaa	aatacgggag	gagcaaataa	ccgttcccga	gctcgataaa	acgtgtgcgc	480
cactatttct	caaaaggaag	tgagtcaaaa	cagtctccac	caaccagac	acaaccaaca	540
attgtcacgg	tgaagggacc	gctaaaatgt	gaatactccg	ttctgaaaaa	aagaaaataa	600
caataataaa	ggcgatgacc	gcaggaaccg	aacatgctca	tctccctctc	aattgttctc	660
atatectaca	tgtttattct	agtggccaat	ctcagaatga	actcaaggaa	agggaggtac	720
aaagccttct	ccactgtag	ctctcatctg	acagtgggtga	tcattgttcta	tgggacattg	780
ttattttatt	acttgcaacc	caagtccagt	catactttgg	ctattgataa	aatggcctca	840
gtgttttata	ccctgttgat	tcctatgctg	aatccgttga	tctacagcct	aaggaacaaa	900
gaagtaaaag	atgctctaaa	gagaacttta	accaatcgat	tcaaaattcc	catt	954

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

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gacatgcagt	ctcatagcag	agtcacccct	tatgcgggct	gcctgacacg	gatgtctttc	120
ttggctcctt	ttgcatgtat	agaagacatg	ctcctgactg	tgatggccta	tgactgcttt	180
gtagccatct	gtcgccctct	gcactaccca	gtcatcatga	atcctcacct	ctgtgtcttc	240
ttcgtttttg	tgctcttttt	ccttagccctg	ttggattccc	agctgcacag	ttagattgtg	300
ttacaattca	ctttcttcag	taatgtggaa	attgctaatt	ttgtctatga	gccatctcaa	360
cttctcaacc	ttgactgttc	tgacaccgtc	atcaatagca	tatttatata	tttcgatagt	420
actgtttggg	tttcttccca	tttcagggat	cctttgtctt	agtataaaat	tgtccctctc	480
attctaagga	tgtcatcgtc	agatgggaag	tataaagcct	tcgccacctg	tggtctcac	540
ctagcagttg	tttgctgatt	tgatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	600
tcaccacccc	ccaggaatgg	tgtggcgggc	tcagtgatgt	acgtgtgtgt	cacccccatg	660

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgattttctat	cacgtgcacc	cagctcatte	accaacccat	gtattttctc	180

ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgacccc	caaattaatg	240
gttgacttac	tggcagaaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accaccatt	tttttggagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttggtg	tactggggga	tttatacatt	ctgccagtca	gtttcttctc	480
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cctttgctga	aattggcctg	ttctaata	cacatgatag	gtctcttagt	cattgcta	600
tcaggcttaa	ttgctttggt	gacatttgtt	gtcttggtgt	tgtcttatgt	ttttatattg	660
tataccatca	gagcatactc	tgcagagaga	cgcagcaaag	ctcttgccac	ttgtagttct	720
catgtaattg	ttgtggctct	gttttttgtc	cctgcattgt	tcatttacat	tagaccggtc	780
acaacattct	cagaagataa	agtgtttgcc	cttttttata	ccatcattgc	tcccatgttc	840
aacctctca	tatacacgct	gagaaacaca	gagatgaaga	acgccatgag	gaaagtgtgg	900
tgttgtcaaa	tactcctgaa	aagaaatcaa	ctt			933

&lt;210&gt; 970

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g820 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 970

cggaacttct	ctttcttaga	aatctcattt	acaaccgtat	gcatccccag	atctctgggg	60
gcaattatca	ccaggaataa	gactatttcc	tataacaact	gtgcagccca	actctttttc	120
tttatcttca	tgggggtgac	tgaattttac	attttaactg	ccatgtccta	tgaccgctat	180
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ctccagctgg	actactgtgc	ttccaacgtc	attgatcact	ttgcatgtga	ctattttccc	360
ctcttacaac	tatcttggtc	agatacatgg	ctcctagaag	taattgggtt	ttactttgct	420
ttggttactt	tgtgtttcac	tttggcatta	gtgattttat	cttacatgta	cattatcagg	480
accattttga	gaatcccgtc	tgccagtc	agaaaaagg	ctttctccac	ttgttcttct	540
cacatgattg	tcattttccat	ttcttatgga	agctgtatat	tcatgtatgc	taatccatct	600
gcaaaagaaa	aggcatcatt	gacaaaagga	atagctattc	tcaatacatc	tgttgccccc	660
atgctg						666

&lt;210&gt; 971

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g821 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 971

ataattttgt	gttttttcat	cataggtaac	tctcaggata	attcccaa	gactttgatg	60
gataacattt	cagaagtga	agaattcggt	ctcgtggggt	taacagatgt	cctagagctt	120
caggctccctt	tatttatcat	ctttactgtc	atttatctca	ccactctggg	tgggaacttt	180
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ggcaaactct	ctctgggtga	cagtgtttgt	cctgctagtc	actggctcct	acatctgtgg	300
actctttcaa	tcctccatcc	atgttgcttt	tactttccat	ctctccttct	gtcattctaa	360
tgtggttaat	cacttttttt	gtgatattcc	accactctta	gctctttctt	gctctgatat	420
ttacgcacat	gagattgtgc	tcttcata	ggcagcattt	aatatctttt	tcactctctt	480
gattatcttg	aactcttatg	tttttatttt	tattgctatc	ctgaggatgc	attcagctga	540
gggacaaaag	aaggtctttt	ccacctgtgc	ctatcacctc	actactgttt	ccatcttcta	600
tgggacaatc	acctttatgt	acttacagcc	aagttctggg	cattccatgg	acacagacaa	660
aatctcatct	gtgttctaca	ccatggatcat	ccccatgctt	aacctcttag	tctatagcct	720
gaggaacaaa	gaagtccaga	gtgcattcaa	gggtgggtatt	ggaaaagcaa	agtcttcatt	780
gggcttagcc	tactatttta					799

&lt;210&gt; 972

<211> 946  
 <212> DNA  
 <213> Unknown (H38g822 nucleotide)

<220>  
 <223> Synthetic construct

<400> 972

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tccctgaatt	tcaggttctt	ctcttccttc	tcttcctcct	cttctacttg	atgatcctct	120
gtggcaacac	agccatcatc	tgggttgtgt	gcacatacag	cgttctccga	accccaatgt	180
atttcttctt	gtccaacctg	tcctttgtag	agatctgcta	caccaccgtt	gtgggtgccct	240
tgatgtcttc	caacattttt	ggggcccaga	agcccatcc	attggctgga	tgtggggccc	300
aaatgttctt	ctttctcaca	cttgggtggt	ctgactgttt	cctcttggcg	atcgtggcct	360
atgaccgcta	tgtggccatc	tgccaccctt	tgcactacc	ctcatcatga	cctgcaatct	420
gtgctgtcag	atgctgggag	gcgctgtggg	cctggccctc	ttcctctccc	tgcagctcac	480
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ctatgtcgtg	agcatcctcg	tgttgaccgt	ccccttcttg	ctcatctgcg	tctcctacgt	660
gttcatcacc	tgtgccatcc	tgagcatccg	ttctgctgag	ggccgccacc	aggccttctc	720
cacctgtctc	tcccacctca	ccgtggctct	gctgcagtat	ggctgctgtg	ccttggcata	780
cttgcatacc	cagtccagct	cctctgcaga	tgaggatcgc	cagtttgccc	ttgtttacac	840
ctttatcaca	ccattactca	accctttgat	ttacaccctt	aggaacaagg	atgtcaaagg	900
tgcccttgaa	aaaagtgtc	agtaccaaag	ggacacctga	gtcctt		946

<210> 973  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g823 nucleotide)

<220>  
 <223> Synthetic construct

<400> 973

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ctgcaggtec	ccttctttat	catgtttgtt	ctcatctatc	tcatcaatgt	agttggaaac	120
ttggggatga	tcattttgat	tctctggtac	tctcagctcc	acaatccaat	gtacttcttc	180
ttcagtaate	tgtctctggt	agactttttt	tactcttcag	ttgtcactcc	aaaggtcatt	240
actgggctcc	ttagagaaga	caaaatcatt	tcctatactg	tgtgggctac	tcagacattc	300
ttttctgatt	cctttgccag	tgtggtaaat	ttattattgg	ccttaatggc	ctctggccac	360
tatgcagcag	tgtgcaaacc	cctgcattac	accaccacca	tgatgacaag	tgtgtgtaca	420
tgtctggcca	taggttgata	cgttgggtgt	ttcctgaatg	cctccattca	cactggggaa	480
acattcagtc	tctttctgta	tgtccagtga	agtcacatcac	tttttctgtg	agggtccagc	540
agtcattggt	ctgtcttgtc	ctgatagaca	tgtgaatgta	gtggttcttg	tttatgtaac	600
cagctcaata	tcctctttgc	ccttctagtt	atcttgatat	cctacttatt	gatgtttatc	660
accatcctaa	agatgcactc	aactgcagga	taccagaagg	ctttggccat	ttgtgcctct	720
cacctcactg	cagttgccat	cttctatggg	actattatct	tcatgcatat	acagcccagc	780
tccagtcatt	ccattgacac	agacaaaatt	gcagctgtgt	tttatactat	tgtcttcccc	840
atgggtgaacc	atgtggtcta	aagattgaag	aacaagggtga	agagtacatt	caagaaaatt	900
gttgagaagg	taaaattgtc	cctaggattg	tgagtt			936

<210> 974  
 <211> 954  
 <212> DNA  
 <213> Unknown (H38g824 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(954)



&lt;223&gt; n = A,T,C or G

&lt;400&gt; 974

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aaggccctgc	agggccccc	gttctgggtg	gtgcttctgg	tctacctggt	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaactctc	agtgggtggag	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcattgt	cctgggcatc	tcggagtgtc	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgctatt	ccaccctctt	gagccacagg	420
gcctgcattg	ccatgggtgg	tacctcctgg	ctcacaggca	tcatacacggg	ccaccaccca	480
tgctccctc	atcttctctc	taccttttctg	cagccaccgc	atcatcccgc	actttctctg	540
tgacatcctg	ccagtactga	ggctggcaag	tgctgggaag	cacaggagcg	agatctccgt	600
gatgacagcc	accatagtct	tcattatgat	ccccttctct	ctgattgtca	cctcttacat	660
ccgcatcctg	ggtgccaatc	tagcaatggg	cctcaccag	agccgccgca	agtcttctcc	720
acctgtctct	cccataggct	cgtgggtctct	ctcttctttg	ggacagccag	catcacnnac	780
aaccggccgc	aggcaggctc	ctctgaaacc	acagaccgcg	tcatcagtct	cttcnacaca	840
gtcatcacac	ccatgctcaa	ccccatcata	aacaccacg	ggaacaagga	cgtgaggagg	900
gcctgcgggt	acttgggtgaa	gaggcggcgc	ccctgcgcgg	gaaggggctc	gggt	954

&lt;210&gt; 975

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g825 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 975

atggagacaa	agaattatag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aaccctaagc	tgcagaaacc	tctctttgcc	atcttctctca	tcattgtacct	actcaactgcg	120
gtggggaatg	tgctcatcat	cctggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagattatct	cttatgtggg	ctgcctgate	300
cagatgtact	tcttcatggc	atttggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtgggttat	gaaaccatgg	420
cattgcctac	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacacccagg	ctgtgctaaa	gctctcctgc	tctgacacat	ccctccagcca	gatgggtggg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttctctgt	gtaccatctt	ctcctacctg	660
caaatcatcg	tcactgtgct	cagaatcccc	tctgcagcca	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgtagtggc	ctgttctatg	ggagtgtcat	ctatgtctat	780
tttaggcctc	tgtccatgta	ctcagtgatg	aagggccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaaaagg	900
ggtttgaaga	aattaagaca	cagaattttac	tca			933

&lt;210&gt; 976

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g826 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 976

atgaaaaata	aaaccgtggt	aactgagttt	atccttctgg	gtctaacaga	tgtccctgaa	60
ctccagggtg	cagttttcac	ctttcttttc	cttgcgtatt	tactcagcat	ccttggaat	120
ctgactatcc	tcattcctcac	cttgcctggac	tcccaccttc	agactcccat	gtatttcttt	180
ctccggaact	tctccttctt	ggaaatttcc	ttcacaaaca	tcttcattcc	aagggtcctg	240
attagcatca	caacagggaa	caagagtatc	agctttgctg	gctgcttcac	tcagtatttc	300
tttgccatgt	tccttggggc	tacagagttt	taccttctgc	tgccattcct	atgaccgcta	360

tgtgccatct gcaaactgat gactatgcac

390

&lt;210&gt; 977

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g827 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 977

atggagataa	agaactacag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aacctcagc	tgcagaaacc	tctctttgcc	atcttcctca	tcatgtacct	gctcgtgcg	120
gtggggaatg	tgtcatcat	ccgggccatc	tactctgacc	ccaggctcca	cacctctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aaggttatct	cctatgtggg	ctgcctggcc	300
cagatgtact	tctttatggc	atttgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tgggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccacgg	420
cattgcctgc	tcatgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgttt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacaccacgc	ctgtgctaaa	gctctcctgc	tctgacacat	cctccagcca	gatggtggtg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttcctgt	gtatcatctt	ctcctacctg	660
cgaatcatgg	tcactgtgct	cagaatcccc	tctgcagccg	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgcagtagcc	ctttctatg	ggagtattat	ttatgtctat	780
tttaggcccc	tgtccatgta	ctcagtgggt	agggaccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaagagg	900
ggtttgaaga	aattacagga	cagaattttac	cgg			933

&lt;210&gt; 978

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g828 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(939)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 978

atgccaaata	agatttggtg	gactgagttc	ttcctcacia	ggcctgacgg	attacaaaag	60
agctttcagg	tggctgtttt	tctgctccct	gatgcttgcc	ataccttggtg	actgtctctg	120
ggaacctgaa	tcacatcatg	ccatgacctt	gctggacacc	cgcacgcaga	catctatgta	180
cttattttct	cagaatctgt	cctgcttaga	aatttggtcc	agacagtcac	cgtgccaag	240
atgctgctca	acattggccat	ggggaccaag	accgttagct	ttgctgggtg	cattaccacg	300
gactttttcc	acatcttctg	ggggccacag	agttcttccct	cctgacagcc	atggcctatg	360
accagtatat	tgccatctgc	aagccccctc	actaccccat	gctcataagt	agtagagtct	420
gcacacagct	catcctcacc	tgctggctac	taggtttctc	cttcatcatc	atgcctgtca	480
tcctgaccag	tcagcttcca	ttctgtgata	cccacatcaa	gcatttcttc	tgtgactaca	540
cgctctctaat	ggaggtgggtc	tgacgtgggc	caaaggtgct	ggagatgggtg	gattttaccc	600
tggccttagt	agcactgttt	ggcaccttgg	tactcatcac	cctgtcctat	gtccagatca	660
ttccagacaat	tgtcagaatc	cccgtgttcc	aggagaggaa	gaaggctttc	tctacctgtt	720
cctctcatgt	cattatgggtt	accatgtggtt	atgacagctg	cttctttatg	tatgtcaagc	780
cctctccagg	aaagtgggtt	gatgtcaaca	angggagtgt	ctctaataca	tacaattatt	840
gccccactgt	taaatccctt	catctgtact	ctgaggaacc	aacaagttaa	gcaggtaatg	900
aaagacctag	tcagaaaaat	gactttgtcc	gaaaaataaa			939

&lt;210&gt; 979

&lt;211&gt; 951

&lt;212&gt; DNA

<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

atgaactcag	agaacctcac	ccggggccgcg	gttgcccctg	ctgaattcgt	actcctgggc	60
atcacaaate	gctgggacct	gcgtgtggcc	ctcttcctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcatggatgc	ccggctccac	180
acacctatgt	acttcttctt	ggccaacctc	tccctgctgg	atgcctgcta	ttcctccgcc	240
atcggcccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgccctcc	agatgtttgt	ctttgcaggc	ctggctgata	ctgagtgttg	cttgctggca	360
gccatggcct	atgaccgcta	cgtggccatc	agaaacccac	ttctctatac	aacagctatg	420
tcgcagcgtc	tatgcctggc	cttgctggga	gcatcaggcc	tgggtggggc	agtgagtgcc	480
tttgttcaca	caacctcac	cttcgcctg	agcttctgcc	gctcccggaa	gatcaatagc	540
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ctccttctct	tcgccatctg	tggcttcac	cagacagcca	cgggtgttagc	tatcacggtg	660
tcttatggct	tcactgctgg	ggctgtgatc	cacatgcgct	cggctcgagg	cagtcggcga	720
gcagcctcca	ccggtggttc	ccacctcaca	ccggtggcca	tgatgtacgg	gacactcatt	780
ttcatgtacc	tcgcgccag	ctccagctat	gccctggaca	ctgacaagat	ggcctctgtg	840
ttctataccc	tggtcatccc	gtctctcaac	ccactcatct	acagcctccg	caataaggag	900
gtcaaggagg	ccctcaggca	gacctggagc	cgattccact	gtccagggca	g	951

<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

atggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tcctcctggg	gaacttgtcc	tgtctggaga	tctgggtatac	ctctaacatc	240
atccccaaaa	tgttgcctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcatcaggct	agctgctggc	tcttgggtct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgcctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcactct	tcttgcctgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataacctg	tgccctcagc	caactcatcc	caactcttgc	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgcaccccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgagggaag	aagtcagggtg	tttgcctt		948

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

gagtaaatgg	gaacaagtaa	taatgttaca	gaatttgtcc	tcccaggcct	ctctcaggat	60
cctgatgtgc	aaaaagcatt	atttgtaatg	tttttactca	catacaatgt	gactatgggtg	120
ggcaaccttc	tcattgtggg	gaccattatt	gccatcgcc	ccttgggactc	cccagtgtcc	180

ttcttcctcg	catgcctgtc	at ttattgat	gctgtatatt	ccacttcctt	ttccccctaa	240
ttgatgatag	acttactctg	tgataaaaaa	gactgtttct	ttcctggctt	gcatgggcca	300
gctatttata	aactacccat	ttgggtggat	tgaggctctt	cttttgggtg	gtatggcctg	360
tgatcactat	gtggacatct	gtaagctact	gcactatttg	accatcatga	actggcaggt	420
ttgcacctc	ctgtttatgg	tggtgtgac	tgagggtttt	tgcattctat	gtttcaaatt	480
gttggtgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccattt	tgtgacatgt	540
acccattatt	ggaaatggtg	tgcactgaca	cttactttat	aggcctcact	gtgattgcca	600
atgggtggagc	agtctgtatg	gtcatcttca	tccttctact	aatctcctat	ggagtcaccc	660
taaactccct	taaaacttat	agtcaggaag	gcgggcataa	agccctgtct	acctgcagct	720
ccaacttacc	tgttgtgtcc	ccttttttga	tcctgttatt	ttcatctatg	ttagacctga	780
ttcaaacctt	cctattgata	aattcatgac	tgtgttttat	acaattatca	cacctatgtt	840
gaatccatta	atatacacac	tgagaaattt	agaggtgaga	attgctgtga	aaaatctctg	900
gtgtaaaaac	taaactatag	taaga				925

&lt;210&gt; 982

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g832 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 982

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atccttttct	tttttgggtc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacatttat	cttcttgatc	tggtgtctct	cctacagttc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcatgatac	agatattttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgctgtctcat	aaccatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tactttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagttagt	agttttcact	gtgattttcc	ttatgtcatg	540
aaactttgctt	gtgtagacac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatactata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttcctt	ttgtatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgcaggttct	900
agcaggatgt	cataataaat	ggtgcataac	cagagtgcac	gatgattcag	tctcacca	958

&lt;210&gt; 983

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g833 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 983

atggaaggaa	taaataaaaac	tgcaaagatg	cagtttttct	ttcgtccatt	ctcacctgac	60
cctgagggtcc	agatgctgat	ttttgtggtc	ttcctgatga	tgtatctgac	cagcctcggt	120
ggaaatgcta	caattgcagt	cattgttcag	atcaatcatt	ccctccacac	ccccatgtac	180
tttttctctg	ctaactctgc	agttctagaa	atcttctata	catcttccat	cacccatttg	240
gccttggcaa	acctcctttc	aatgggcaaa	actcctgttt	ccatcacggg	atgtggcacc	300
cagatgtttt	tctttgtctt	cttgggtggg	gctgattgtg	tcctgctggt	agtcattggt	360
tatgaccggt	ttatagcgat	ctgtcaccct	ctgcgataca	ggctcatcat	gagctgggtc	420
ttgtgtgtgg	agctgctggt	aggctccttg	gtgctggggg	tcctgttgct	actgccactc	480
accattttta	tcttccatct	cccattctgc	cacaatgatg	agatctacca	cttctactgt	540
gacatgcctg	cagtcatgcg	cctggcttgt	gcagacacac	gcgttcacaa	gactgctctg	600
tatatcatca	gcttcatcgt	ccttagcatc	cccctctcat	tgatctccat	ctcctatgtc	660
ttcatcgtgg	tagccatttt	acggatccgg	tcagcagaag	ggcgccagca	agcctactct	720

acctgctctt	ctcacatctt	agtggctctc	ctgcagtatg	gctgcaccag	ctttatatac	780
ttgtccccc	gttccagcta	ctctcctgag	atgggccggg	tggtatctgt	ggcctacaca	840
tttatcactc	ccattttaaa	ccccttgatc	tatagtttga	ggaacaagga	actgaaagat	900
gccctaagga	aagcattgag	aaaattc				927

&lt;210&gt; 984

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g834 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 984

gattcagtgg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttgg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatatct	tgctggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tggtgctgct	gatagtcatg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttc	ctcgggttat	taaacttgca	tgcattggaca	cttatgggct	agaatttgtg	600
gtcactgcca	acagtggatt	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatac	660
atttttatct	tggtcactgt	ccaacgacat	tcctcaaatg	atztatccaa	agcattcttc	720
acttcgtagg	ctcacatcac	cgtagtgggt	ttgttttttg	ctccatgcat	gtttctctac	780
gtgtggcctt	tcctactaa	gtcattggat	aaattttttg	ccatcatgaa	ctttgttgtc	840
accctgtct	taaatcctgc	catctatact	ttaaggaaca	aagatatgaa	gtttgcaatg	900
agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgcca	tggacca				987

&lt;210&gt; 985

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g835 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 985

tccatgtact	tcttcctgac	aaactttgca	ggtctggaga	tcttctactt	tttcaccatt	60
gcccctctga	ctctggccaa	tgctctaccc	atggggagaa	acctcatctc	cctgccccgc	120
tgtggaggcc	agatgttctt	cttcactctc	ctgggaaggg	ctgactgcat	cctgctggcc	180
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ttctactgtg	atgtcctccc	tgctcatgaga	ctggcctgtg	cagataacctg	ggtccatgag	420
gccactatgt	ctatggtcag	caccaccttt	ctcaccgtcc	ccttcctgct	catcactctt	480
tcctatgtct	ccatcatggc	cgccatcttg	aagatttgc	ctgcagaggg	gaggcacaag	540
gccttctcca	cctttcctcc	cacctgactg	tggttctcct	ccaggactga	tgtacacgcc	600
tcgccttctt	gtgtccacgc	tctagctact	atcctgagag	gggccaggca	gtgtctgtgg	660
tttacacctt	cattaccctt	gtgctgaacc	ctttgatcta	cagcatgagg	aacacagaac	720
ttaaggatgc	tttgaagaga	gcaatgacga	gggtccccgt	gctctaaaca		770

&lt;210&gt; 986

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g836 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 986

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaaactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcactct	cccagtact	tcctgctagc	caacctctca	180
ctcattgac	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctc	cttgttcaga	tatttctcct	tcacttcttt	300
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gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttacc	480
ttctgtggte	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atgggtcattg	ctaacagtgg	tgtgtcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaatagac	catccagcat	660
tgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccc	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 987

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g837 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 987

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atctttttct	tttttgggtc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacattttat	cttcttgatc	tgggtcttct	cctacagtcc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcattgatac	agatattttt	cattttgtgtc	300
atgcgtaaaa	attgagatgg	tgctgctcat	aacctatggc	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	ttggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagatac	ttacaaacta	gaggtttag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatcctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttggtc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgacaggtct	900
agcaggatgt	cataataaat	ggtgcatatc	cagagtgcac	gatgattcag	tctcacca	958

&lt;210&gt; 988

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g838 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 988

ctttctatatt	gcttctttct	ttgcatattt	tcagctgata	tttaattctat	gctagccatg	60
gaacaaaata	atggcactga	agtgactgaa	ttcattctcc	tgggatttgc	tggtcaacac	120
aagtcttggc	atatcctctc	catagcattt	ctagcaatct	atgtgggttac	cccagtaggt	180
aatatttgaa	tatcctact	tatcaaaatt	gatgcttctc	ttcatatccc	catgtaaatt	240
ttcctccaac	acttggcatt	tgttgatctc	tgttacacct	ctgctatcac	tcccaagatg	300
ttgaaaaact	ttgtagaaac	aaaaaaatct	atctcatgta	taggatgtat	ggtgcaatta	360

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ctagtttatg gtacttttga acaagtgact gctacatcct ggctgctatg gcagtagacc 420
ggtatgtggc cttctgtaac ccactccatt atccaggggt tatgtcccag agactctgca 480
ttaagctatt agttagttca tatgtcatgg gtttcctaaa tgcctctata aacataagtt 540
tcaacttttc attgaacttc tgcaaatcca aaacaattaa tcaacttttc tgtgatgaac 600
ctccaattat tgcctacca tgctccaata ttgacctcaa catcatgtta ttaacagtat 660
ttgtgggatt aaatttgatg tgcactgtga tgggtggcat catttctgc atatatgtcc 720
tgggtggcat cctgaggata tcttctgctg caggggaagaa aaaagtctct ctacatgtgc 780
ctcccacctg acagcagtca ccatttttcta tgggggttctc tcttacatgt atctatgcca 840
tcgtattaat gagtctcaaa aacaagaaaa agtggcctct gtgttttatg gcattattat 900
tcccattgta aacccttga ttacagcca gagaaaccaa gatgtgattg aagccataaa 960
actaacagaa aaaaagtatt tc 982

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&lt;210&gt; 989

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g839 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 989

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atgatttctt tccttgtacc aggtctaatt gaagaggaaa accagagggg agtgggtacac 60
ttccacttcc acttcttttc aacagacctg gtgggtggctt cttttataat tgtggccttg 120
atgttgacc aagaagcctt gttggacctc tcaccttttg gccacagtc tggcaagatc 180
cttccctcca tattccaatg tatttatttt tatttttttg gcattgacta tgttggaat 240
tggctactcc accaacattt ctctccaac actggctacc gtcctttaca tggggaagat 300
gcttatctcc ctccctggct atggaactca gatgctcttt gtcaccttt tgagaggatc 360
tgagtgtgtc ttgcttgctg tcatggctta tgataggtat ataaccatct gtcacccatt 420
caattacaat ctcatcatga gtgggtagct ctgtgggcag atgacttttg gctctttgag 480
gctgggatcc ctgttgtcac tgtttttgac tatgttgatc tgacaccctc cattctgttg 540
cctaataaaa cctaccactt ctctctgtgac atgcccacag caagtgcctg gtcctgtgag 600
acaccacatg catgagtcag ctctctgact tccgtgtggc caccatcacc atccccttc 660
ttcctccttg tctgcctccc ctatggctgc cttgcagcca ccatcttgag gatgcattca 720
gctaagagaa agcactaggc ctctcttacc agttcctccc acctcattgt ggttctcctg 780
aagtattggt gttgcatcct catctgcctt tgccccagct ctagttactc cccagaggag 840
ggctgggagg tatctcttgt tcacatgttt ttctcccggt gtggaatccc ttgatctata 900
gcgtatggaa ccaagacgta actgatgcag tagagagact tgtggcaaga atgtccttgt 960
tctaacagcc agaaatattc cttcttaaaa aatatttccc taacta 1006

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&lt;210&gt; 990

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g840 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 990

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gattcagtg accaagtaaa tgactctctg gtaacagaat ttgtattact tggacttgca 60
caatccttgg aatgcagtt ttctcttttt ctctctctct ctttattcta tgtgggaatt 120
atcctgggaa acctcttcat tgtgttcaca gtgatctttg atcctcactt acactcccc 180
atgtatatcc tgttgcccaa cctatcgctc attgacttga gcctttcatc taccacagtt 240
cctaggttga tctacgatct ttttactgat tgtaaagtta ttctctcca taattgtatg 300
atacaaaagt tctttatcca tgttacagga ggagtgaata tgggtgctgct gatagtcatg 360
gcataatgata ggtacactgc gatctgcaaa cctctccact atccaactat tatgaacccc 420
aaaatgtgca tgttttttgg agcagcagct tgggtcattg ggggtgattca tgctatgtct 480
cagtttgttt ttgtcataaa tttacccttc tgtggccta ataagtggg gagcttttat 540
tgtgattttc ctcggttat taaacttgca tgcattggaca cttatgggct agaatttgtg 600
gtcactgcca acagtggatt catatcgatg ggcaccttct tttctttaat tgtatcatac 660
atttttatcc tggtcactgt ccaacgacat tcttcaaatg atttatccaa agcattcttc 720
acttcgtagg ctcacatcac cgtagtgggt ttgttttttg ctccatgcat gtttctctac 780

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gtgtggcctt	tccctactaa	gtcattggat	aaattttttg	ccatcatgaa	ctttgttgtc	840
accctgtct	taaatcctgc	catctatact	ttaaggaaca	aagatatgaa	gtttgcaatg	900
agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgccca	tggacca				987

&lt;210&gt; 991

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g841 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 991

atgcaatcag	aacaccttgc	agaattttca	gaattcctca	ttttgagcct	ctcaggagat	60
ccagaactgc	agccccttct	tgggctgttt	ctgtccatga	acctgggtcac	agtgccttga	120
aacctgctca	ttatcctggc	catcagttct	gactcccacc	tccacaagcc	tatgtacttc	180
ttactctcca	aattgtccat	ggctgccatt	tgttttgtct	tcacatgat	ccaaaagatg	240
atggtaaacc	tcagggcaca	gagcaaagac	atcctttactc	agccaagtgg	tagtccaatt	300
ccattctaaa	tgtgtagtct	tatcagattt	cttctaattc	agcagaaatc	tgttgtttta	360
atcttcgaat	actcactggg	tctaattctc	ctatttgaat	ctgaagatgt	aaactaatta	420
ttcttttga	tgagcctttc	aaaataattg	aagacagtta	tgctcctttc	ttgataatca	480
ccatactttc	ttcacactaa	ttgatacaca	attgttaata	agtcatggat	tttctactca	540
aacaaccttt	attctatcat	cttatgcttc	tggttatgca	acagttgact	ctcaatgctt	600
tattttattt	ttaaacatga	tgattactat	taacctcttt	gtaagattta	aaaatatctt	660
tatgcacagt	agtatctcaa	taaattacaa	ctattatttt	aaaaaataaa	ataaagggtg	720
tatctatgag	atatat					736

&lt;210&gt; 992

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g842 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 992

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtggtat	ctgactccca	ccttcactct	cccattgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggctgc	cttggttcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtg	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccttac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atgggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaatagac	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattcccat	caagtcatta	780
gataaattcc	ttgtctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 993

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g843 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 993

atggctgcag	gaaatcactc	tacagtgcga	gagttcattc	tcaagggttt	aacgaagaga	60
gcagacctcc	agctccccct	ctttctcttc	ttctcggga	tctacttggt	caccatcggt	120
gggaacctgg	gcatgatcac	tctaatttgt	ctgaactctc	agctgcacac	ccccatgtac	180
tactttctca	gcaatctgtc	actcatggat	ctctgctact	cctccgtcat	tacccttaag	240
atgctggtga	actttgtgtc	agagaaaaac	atcatctcct	acgcagggtg	catgtcacag	300
ctctactttc	tccttggttt	tgtcattgct	gagtgttaca	tgctgacagt	gatggcctac	360
gaccgctatg	ttgccatctg	ccaccctttg	ctttacaaca	tcattatgtc	tcacacacac	420
tgctgctgc	tggtggctgt	ggtctacgcc	atcggactca	ttggctccac	aatagaaact	480
ggcctcatgt	taaaactgcc	ctattgtgag	cacctcatca	gtcactactt	ctgtgacatc	540
ctccctctca	tgaagctgtc	ctgctctagc	acctatgatg	ttgagatgac	agtcttcttt	600
tcggctggat	tcaacatcat	agtcacgagc	ttaacagttc	ttgtttctta	caccttcatt	660
ctctccagca	tcctcggcat	cagcaccaca	gaggggagat	caaagcctt	cagcacctgc	720
agctccacc	ttgcagccgt	gggaatgttc	tatggatcaa	ctgcattcat	gtacttaaaa	780
ccctccacaa	tcagttcctt	gaccaggag	aatgtggcct	ctgtgttcta	caccacggta	840
atccccatgt	tgaatcccct	aatctacagc	ctgaggaaca	aggaagtaaa	ggctgccgtg	900
cagaaaacgc	tgaggggtaa	actgttt				927

&lt;210&gt; 994

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g844 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 994

atggcagcca	aaaactcttc	tgtgacagag	tttatcctcg	aaggcttaac	ccaccagccg	60
ggactgcgga	tccccctctt	cttcctgttt	ctgggtttct	acacggtcac	cgtgggtggg	120
aacctgggct	tgataaccct	gattgggctg	aactctcacc	tgacactcc	catgtacttc	180
ttccttttta	acctctcttt	aatagatttc	tgtttctcca	ctaccatcac	tcccaaatg	240
ctgatgagtt	ttgtctcaag	gaagaacatc	atttcttcca	caggggtgat	gactcagctc	300
ttcttcttct	gcttctttgt	cgtctctgag	tccttcaccc	tgctcagcat	ggcgtatgac	360
cgctacgtgg	ccatctgtaa	cccactgttg	tacacagtca	ccatgtcttg	ccagggtgtg	420
ttgctccttt	tgttggggtg	ctatgggatg	gggtttgctg	gggccatggc	ccacacagga	480
agcataatga	acctgacctt	ctgtgctgac	aaccttgctc	atcatttcat	gtgtgacatc	540
cttcctctcc	ttgagctctc	ctgcaacagc	tcttacatga	atgagctggg	ggtctttatt	600
gtgggtggctg	ttgacgttgg	aatgcccatt	gtcactgtct	ttatttctta	tgccctcatc	660
ctctccagca	ttctacacaa	cagttctaca	gaaggcaggt	caaagcctt	tagtactttg	720
agttccacaa	taattgtagt	ttctcttttc	tttggttctg	gtgctttcat	gtatctcaaa	780
cccctttcca	tcctgcccct	cgagcaaggg	aaagtgtcct	ccctgttcta	taccataata	840
gtccccgtgt	taaacccatt	aatctatagc	ttgaggaaca	aggatgtcaa	agttgccctg	900
aggagaactt	tgggcagaaa	aatcttttct				930

&lt;210&gt; 995

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g845 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(473)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 995

atgggagaag	caaggaacag	gacagtagtc	caggaattta	tcctggaggg	atttctgtct	60
gtccagcatc	tggggaatgt	cttttctctg	gtgcacctgc	tggcatacct	ggcctccatc	120
atggcaaaca	tgctcataat	caccatcacc	tgggtgacc	atcacctcca	gacacctatg	180

tattttcttcc	tcagcagttt	ttccttctgt	gaatgctggt	ttatcaccac	agttattcct	240
aaacttctgg	tcatactttc	tttcaggcag	ggcaaataat	ccccctttct	actaccttgt	300
ctcatgcagt	ccccctttca	tttttatntt	cttgggtcaa	cagtttttct	tcctttaatg	360
gctgtgatgt	cccccttggat	tgatacctgg	ccatttgcaa	gcctctgcat	tactccacca	420
tcatgagcct	gaggactage	ttccacaagg	tcactgcctg	gctttgtcct	ggg	473

&lt;210&gt; 996

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g846 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 996

acagacccac	agaatctaac	aacagatgtc	tcaatattcc	tcgtcctaga	actctcagag	60
gatccagaac	tacagccggg	cctcgctggg	ctgttctctgt	ccatgtgcct	ggatcatggtg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tactttctcc	tctccaacct	gtccttgccct	gacatgggtt	cacctccacc	atggtcccca	240
agatgattgt	ggacatccaa	tctcacagca	gtcatctcct	atgcgggctg	cctgactcag	300
atgtctcttt	ttgccatttt	tggaggcatg	gaagaaagac	atgctcctga	gtgtgatggc	360
cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatta	ttcagccatc	atgaacccat	420
gtttctgtgg	ctttctagtt	ctgttgtctt	gttgctctcag	tcttttagac	tcccagctgc	480
acaatttgat	tgccttgcaa	attacctgct	tcaaggatgt	ggaaattcct	aattttcttct	540
gtgacccttc	tcaactcccc	caccatgcgt	gttggtgacac	cttcaccaat	aacatagtca	600
tgtatttccc	tgctgccata	tttggttttc	ttcccacctc	ggggatcctt	ttctcttact	660
ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggaactat	aaagccctct	720
ctgcctgtgg	gtctcacctg	tcagttgttt	gcttatttta	tggaaacaggc	gttggagggt	780
acctcagttc	agatgtgtca	tcttccccca	gaaagggtgc	agtggcctca	gtgatgtaca	840
cgggtggtcac	ccccatgctg	aacccttcca	tctacagcct	gagaaacagg	gatattaaaa	900
gtgtcctgcg	gcgcctgcac	ggcagaacag	tctaattctca	atatcttatt	atctgttcca	960
ttccttttgt	agtgtgggtt	taaaaaggca	gcaagggtc			998

&lt;210&gt; 997

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g847 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 997

agtcaactgt	cccttatgga	cctcatgtct	atctgcacca	ctctacccaa	gatgatcttc	60
agctacttgt	ctgggaagaa	atctatctct	ctggcagggt	gtggaactca	gatattcttc	120
tatgtgtccc	tgcttgagc	tgaatgtttc	ttgttggtctg	tcattggctta	tgaccgctat	180
gtggctatat	gtcacccctc	tcagtacacc	atcctcatga	atccggaact	ctgtgtcttc	240
atgactgttg	cttccctggac	cttgggggtct	cttgatggga	tcattagtgt	tgacagctgtc	300
ctgtcatttt	cttactgcag	ctctctggaa	attcatcatt	ttttctgtga	tggtgtgtgcc	360
cttttacctc	tatcctgcac	agaaacatct	gcatttgaaa	gactacttgt	catttgtttgt	420
gtggtaatgc	taatctttcc	agtttcagtt	atcatacttt	cctattccca	tgctccttcca	480
gccgtcatcc	acatgggctc	tggggaaagt	cgtcgcaagg	ccttcactac	ctgctcctcc	540
caccggtctg	tggtcggaact	ctactacggt	gctgctatgt	tcattgtacat	gagaccagct	600
tctaaacata	cgccagacca	ggacaagatg	gtgtcggcct	tctacactaa	tctcaccctc	660
atgctg						666

&lt;210&gt; 998

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g848 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 998

cttgccctgca	tagttggata	gaagtttgca	tttattat	ctccaaacca	tcacttcacg	60
ataatgggtca	catttcatttt	agttaacatt	taaaaacatt	cttcaggaaa	cttatccagt	120
gctcttatca	ttttgttcat	tttcatccct	gttggtttctc	tattttttcac	tccatgcgta	180
gttctctatg	tttggccctac	tttgccacca	tcacttgata	aaaatatgtt	cattgttgac	240
tttgttggtca	accctgtctt	gaagcctgcc	acctacatat	tacagaacaa	agacataaag	300
gtagcacttt	gaaatttgca	tgaaaagaga	acttattcca	gc		342

## &lt;210&gt; 999

## &lt;211&gt; 915

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g849 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 999

atggtgactg	aatttcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttccta	60
tttatgttgt	ttttgtatt	ctatggagga	atcggtgttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcactctctt	caagggtgc	cttggttcaga	tatttctcct	tcacttcttt	300
ggtagggagt	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaaccctac	actacactac	aattatgtgt	ggcaacgcac	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttacc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctaggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atgggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtattt	720
cttttgttct	ttggaccatg	tgtcttttatt	tatgcctggc	cattcccat	caagtattta	780
gataaattcc	ttgtctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

## &lt;210&gt; 1000

## &lt;211&gt; 669

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g850 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1000

tccaacctgt	ccttgccctga	catcggtttc	ccctcccca	cggccccaa	gatggttgtg	60
gacatccaat	ctcacagcag	tcatttctct	atgcaggctg	cctgactcag	atgtctctct	120
ttgccatttt	tggaggcatg	gaagagacac	atgtctctga	atgtgatggc	ctatgtccgg	180
ttttagtcca	tctgtcaccc	tctatatcat	tcagccatca	tgaacctcgt	tttctgtggc	240
ttcttacttt	tgttgtcttt	tttttttctc	agtcttttag	acgcccagct	gcacaacttg	300
attgccttac	aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctc	ctgtgacctt	360
tctccactcc	cccactttgc	atgttgtgac	accttcacca	ataacataat	catgtatttc	420
cctgtcgcca	tatttggttt	tcttcccatc	tcggggaccc	ttttctctta	ctataaaatt	480
gtttcctcca	ttctgagggt	ttcatcatca	ggtgggaagt	ataaggcctt	ctccacctgt	540
gggtctcacc	tgtcgggtgt	ttgctgattt	tatggaacag	gcgttgagg	gtacctcggt	600
tcagatgtgt	catcttcccc	gagaaagagt	gcagtggcct	cagtgatgta	cacggtggtc	660
acccccatg						669

## &lt;210&gt; 1001

## &lt;211&gt; 986

## &lt;212&gt; DNA

&lt;213&gt; Unknown (H38g851 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1001

gattcagtg	accaaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttga	60
caatccttgg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatatcc	tgctggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tggtgctgct	gatagtcattg	360
gaatatgata	ggtacactgc	gatctgcaag	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgttttttgg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttggtt	tgtgcataaa	ttaaccttct	gtggccctaa	taatgtgggg	agcttttatt	540
gtgattttcc	tcgggttatt	aaacttgcat	gcattggacac	ttacgggcta	gaatttgtgg	600
tcactgccaa	cagtggattc	atatcgatgg	gcaccttctt	tttcttaatt	gtatcataca	660
tttttattct	ggtcactgtc	caacgacatt	cctcaaatga	tttatccaaa	gcattcttca	720
cttcgtaggc	tcacatcacc	gtagtgggtt	tgttttttgc	tccatgcatg	tttctctacg	780
tgtggccttt	ccctactaag	tcattggata	aattttttgc	catcatgaac	tttgttgta	840
ccctgtctt	aaatcctgcc	atctatactt	taaggaacaa	agatatgaag	tttgcaatga	900
gaaggctgaa	tcaacatatt	ttaaattcta	tggagacgac	ataacacatt	tggttgatga	960
gagcacagga	taaatgccat	ggacca				986

&lt;210&gt; 1002

&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g852 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1002

agtgtgctgt	ctattttctga	gacctattat	accgtggcca	tcaaccccca	aatgctgtcc	60
ggtctctctca	gtcctcaaca	aaccatctcc	atcccaggct	gtgccgctca	gctctttttc	120
tatctcactt	ttggtgtcaa	taaatgcttc	ctgctcacag	ccatggggta	tgaccactat	180
gtggccatct	gcaaccctct	acagtattca	gtcatcatgg	gcaaaaaggc	ttgtatacaa	240
ctggctcagt	gatcctggaa	cattggcctg	agcacagcta	tcattcaggt	gtcttctgta	300
ttcagccttc	ccttctgtga	tgctaatctc	atctccact	tcttttgtga	tatccggccc	360
ataatgaagc	ttgcctgtgc	agacactact	atcaaggagt	ttattacttt	gctcatcagt	420
ctctgtgtcc	ttgttctgcc	catgggtattg	atcttcatct	cctatgtcct	aattgtcacc	480
accatcctca	agattgcac	agctgagggc	ggagaaaaggc	ccttgctact	tggtgcctcac	540
acctcacagt	ggtcattgtc	cactatggcc	gtacttcttt	catctaccta	aaacccaaat	600
cccaaaattc	cctgcaggac	agacttatct	ctgtgacata	cactgttatt	actcctctg	659

&lt;210&gt; 1003

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g853 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1003

atgtctacgt	ctaatacacac	ccagttccat	ccttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ttggattgga	gtcccttttt	tctttgtgta	tcttgttgca	120
ctcctgggaa	acactgctct	cttgtttgtg	atccagactg	agcagagtct	ccatgagcct	180
atgtactact	tccctggccat	gttgatttcc	attgacctgg	gcttgtctac	agccaccatc	240
cccaaaatgt	tgggcattct	ctgggtcaat	accaaagaaa	tatcttttgg	aggctgcctt	300
tctcacatgt	tcttcatcca	tttcttcaat	gctatggaga	gcattgtgtt	ggtggccatg	360
gcctttgacc	gctacattgc	catttgcaaa	cctcttcggt	acaccatgat	cctcaccagc	420

aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcctgtacat	ggttgttcca	480
ctggtgtttc	tccttctgag	gctgcccttc	tgtgggcatc	gtatcatccc	tcatacttat	540
tgtgagcaca	tgggcattgc	cgtctggcc	tgtgccagca	tcaaagtcaa	cattagggtt	600
ggccttggca	acatatctct	cttgttactg	gatgttatcc	ttattattct	ctcctatgtc	660
aggatcctgt	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtgggt	ctcatattgg	tgttatctta	gccittttta	caccagcatt	tttttcatte	780
ttgacacatc	gttttggcca	taatatccca	cagtatatac	atattatatt	agccaacctg	840
tatgtgggtg	tcccaccagc	cctcaatcct	gtaatctatg	gagtcaggac	aaagcagatt	900
cgagagagag	tgctgaggat	ttttctcaag	accaatcac			939

&lt;210&gt; 1004

&lt;211&gt; 877

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g854 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1004

tacatgataa	ccatcttatg	ggaaatatct	aagccagtaa	ataatatattt	tctaacactt	60
tctgtaagat	atcaaatgct	aatcactact	gtgtcataat	tgtaaataaa	attataatat	120
aaattttactg	agtttttctg	agtacctaata	gagttaaaaa	atatgggagc	atatgtagta	180
ctgtgcttgt	atcaatatgg	ataaggtatc	tggaagtctt	ttctgaacat	ctttcggtgc	240
tgctgagatt	attccactga	tggggatggg	ccatggctgc	tatgtgacca	tctgcactgc	300
atgaaaatca	tgactcaata	taggtgtggc	catcttgctg	gaatggcatg	cactggaaga	360
tttatccagg	cacagtttag	atcctctccc	cagtctgact	tcctttctat	aattccaatg	420
tcacaatatg	aatagcccat	tcatatgtga	cttaaacact	ttgttgaagc	tcctctgcat	480
aggtagtatg	atacacttgg	tctctttgtt	gctgccaatg	atgggttcaa	ctgcctgtta	540
aacatcatct	tcttgatggg	ttcttaagtg	gccatcctat	atactttgaa	atcccacagc	600
ttggaggaaa	gatacaaaagc	tctctctacc	tgtgtctctc	acaccaccgt	ggccatctaa	660
tcttttgtgt	tctgtatact	tgtttatctg	tgcccagtga	cccttcccca	gtcagtaaaag	720
cagtggctgt	gctttacacc	atgataacgc	ctacattaaa	ccctttagtc	taaccctcag	780
aatgacagag	gtgaaaagtg	ttgagaaact	tctgggtcaa	aagatgactt	gaagagagaa	840
ataatccaaa	cataagatga	ttttactctt	tcaatgg			877

&lt;210&gt; 1005

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g855 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1005

atggagaaga	aaaagaatgt	gactgaattc	attttaatag	gtcttacaca	gaaccccata	60
atggagaaaag	tcacgtttgt	agtatttttg	gttctttaca	tgataaacact	ttcaggcaac	120
ctgctcattg	tggttaccat	taccaccagc	caggctctga	gctcccccat	gtacttcttc	180
ctgaccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtggattcct	ttcaagagaa	gaaaatcatc	tcctttaatg	gggtgatggc	tcaagcctat	300
gcagaacaca	tttttggtgc	tactgagatc	atcctgctga	cagtgatggc	ctgtgactgc	360
tatgtggcca	tctgcaaac	tctgaactac	acaaccatta	tgagccacag	cctgtgcatt	420
ctcctggtgg	cagtggcctg	gggtgggagga	tttcttcatg	caactattca	gattctcttt	480
acagtatggc	tgcccttctg	tggccccaat	gtcataggcc	acttcattgt	tgacttgtac	540
ccattgttaa	aacttggttg	catagacact	catacccttg	gtctctttgt	tgctgtgaac	600
agtgggttta	tctgcttatt	aaacttcctt	atcttggttg	tatcctatgt	gatcatcttg	660
agatctttaa	agaacaatag	cttggagggg	agggtgtaaag	ccctctccac	ctgtattttct	720
cacatcatag	tagttgtctt	attctttgtg	ccctgtatat	ttgtgtatct	gcgctcagtg	780
accactctgc	ccattgataa	agctgttgct	gtattttata	ctatggtggg	cccaatgtta	840
aatcccgtgg	tctacacact	cagaaatgct	gaggtaaaaa	gtgcaataag	gaagcttttg	900
agaaaaaaag	tgacttcaga	taatgat				927

<210> 1006  
 <211> 738  
 <212> DNA  
 <213> Unknown (H38g856 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1006  
 tgtattcaac aacattgata tccactttgt ctctgcatgt tctcctttta ttttaatttg 60  
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120  
 ttggtataaa gtaaggtatc tgattaacca aatttacact aaagccaatt ggccttttca 180  
 tggattataa cactatgcac aaccactcca tactcaaaca tgcatttctt tctccaatgt 240  
 tatatgatgc agcacctagc tctttacagg acattttttt cttggtgggt cacagatttt 300  
 ccttctgttg gtgatggcct agggcactat agggccatct gcaagtcctt gcagtatttg 360  
 gttgtcatga agcaatggct gtgtgttggt ctgctgggtg tgcctgggc tggaggattt 420  
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgtc 480  
 attggtcatt ttatttgtga catggacccc ttaatgaagc ttgtctgtga ctacacactc 540  
 aacagatttg cctattttgc aggtcatgat taaatactag gttttatgta tttcacttat 600  
 gctcagactg gactgtttcc ttttggtgat tgcacctcat tattcttttg tcattttttc 660  
 cctagaggac ttggttctat aaatcttgct atacatagtt attatccctg tggcatctct 720  
 agagatacgg agcctacc 738

<210> 1007  
 <211> 786  
 <212> DNA  
 <213> Unknown (H38g857 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1007  
 ctaattgtag tcaccgtaac tgtcagttag accctgggct caccaatgta cttcttttctt 60  
 gctggccttat catttataga tatcatttat tcttcatcca tttccacag attgatttca 120  
 gacttgttct ttgggaataa ttccatatcc ttcccatctt gcttggccca gctctttaca 180  
 gagcaccttt ttggtgggtc agaggtcttt cttctgttgg tgatggccta tgaccttgca 240  
 ttacttgggt atcatgagac aatgggtgtg tgttttgcgt ctggtagcgt cctgggttgg 300  
 aggatttctg cactcagtat ttcaacttag tgttatttat gggctcccat tctgtgacct 360  
 caatgtcatt gatcattttt tctgtgatat gcacccttta ttgaaactgg tctgtactga 420  
 taccatgtt attggcctct tagtggtggc caatggagga ctagggtgca ctattgtgtt 480  
 tctgctctta ctcatctctt atggtgtcat ctgcactctc taaagaacct tagtcagaaa 540  
 gggaggtgaa aagccctctc aacctgcagt tcccacataa ctgtggttgt tttcttcttt 600  
 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660  
 agtgtgtttt atacagtcac aactccaatg ctgaaccctt taatctacac tctgagaaat 720  
 tctgagatga caagtgcata gaagaagtc tggagaagag acttcatatc aagtagtaca 780  
 taagtg 786

<210> 1008  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g858 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1008  
 atgagacaga ataataatat tacagaattt gtcctcctgg gcttctctca ggatctggat 60  
 gtgcaaaaag cattatttgt catattttta ctcacatact tggtagacgt ggtggggaac 120  
 ctgctcattg tggtagctat tattgccagc ccttctctgg gctcctcaat gtacttcttc 180  
 cttgcctgcc gtcatattat agatgctgca tattccacta caatttctcc caaattgatt 240  
 gtagacttac tctgtgataa aaagactatt tctttcccag cttgcatggg ccagttattt 300

atagaccagc	ctggatggcg	gagctgaggt	cgtgcttctt	gtgggtgaagg	cctgtgatca	360
ccatgtggac	atctggaagc	cactgcgcta	tctcgactat	catgaatcga	cagggctgaa	420
tgcggctgct	cgtggctgtc	gtcgactcg	aggtgttctg	cattcgctgt	ctcatattgt	480
gagtgtgtat	acagtctcgc	ctactgtggc	cccaatgtca	ttgactactt	tgtctgtgac	540
atgtacccag	ttattggaac	tggtatgcac	tgacacctac	tttattggcc	ttactgtttt	600
tgtcaatggt	ggaacaatct	gtatagtcgt	cttcaccctt	ctactaatct	cctatggagt	660
catcctaaac	tcccttaaaa	cttacagtca	agaagggagg	cataaagtc	tgtttacctg	720
cagctccac	attatcgtct	ttgccctctt	ttttgttccc	tgtattttca	tgtatgttag	780
acctgtttca	aacatccttt	tgataaatc	ctgacagtgt	tttatacagt	tatcacaccc	840
atgttgaatc	ctttaatata	cacattgaga	aattcagaga	tgagaaatc	tgtagaaaca	900
ctcttgtgta	aaaagttaac	tgtattagag				930

&lt;210&gt; 1009

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g859 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1009

atgcagagga	gcaatcacac	agtgactgag	tttatactgc	tgggcttcac	cacagaccac	60
gggatgcagc	tgggcctctt	cgtgggtgtc	ctgggcgtgt	actctctcac	tgtggtagga	120
aatagcacc	tcacgtgtt	gatctgtaat	gactcccacc	tccacacacc	catgtatttt	180
gtcgttgaa	atctgtcgtt	tctggatctc	tggtattctt	ctgtctacac	cccaaagatc	240
ctagtgtat	gcatctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttcttctctg	cagggctggc	ctatagttag	tgtgtcttac	tggctgcat	ggcttatgac	360
cgctacgtgg	ccatctccaa	gcccctgctt	tatgccagg	ccatgtccat	aaagctgtgt	420
gcattgctgg	tagcagtctc	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
aaaacgtttt	cctttaactt	ctgccgtgaa	aacatcattg	atgacttttt	ctgtgatttg	540
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cctctggcct	ccaatgtcat	ctgcccgcga	gtgctcatcc	tggcctccta	cctctttatc	660
atcaccagtg	tcttgaggat	ctcctctctc	aagggctacc	tcaaagcctt	ctccacatgc	720
tcctcccacc	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	tgaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	tccca					915

&lt;210&gt; 1010

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g860 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1010

atgatctgtg	aaaatcacac	cagagtcact	gaatttattc	ttcttggttt	tacaaacaac	60
cccagatgc	aagtttccct	ctttattttt	ttcctggcca	tttatacagt	cactttgttg	120
ggcaactttc	ttattgtcac	agttaccagt	gtggatctcg	cacttcaaac	acccatgtac	180
ttctttcttc	aaaatctgtc	acttcttgaa	gtatgtttca	ccttggttat	ggtgccccaa	240
atgctttag	atctagtgtc	cccaaggaaa	attatctctt	ttgtgggctg	tggtagccag	300
atgtacttct	tcttcttctt	tggcagttct	gaatgtttcc	ttctctccat	gatggcttat	360
gatcgctttg	tggccatctg	taaccctctc	cattattcag	tcataatgaa	caggctcccta	420
tgcttgtgga	tggccatagg	ctcttggatg	tccggtgttc	ctgtgtctat	gctacagaca	480
gcttggatga	tggcccttcc	tttctgtgga	ccaaatgccg	tggaccactt	tttctgtgat	540
ggccccccag	tgttaaaact	agtcacagt	gatacaacca	tgtatgaaat	gcaagcactt	600
gcctccacac	tcctgtttat	catgtttccc	ttttgtctca	ttttgggttc	ctacacccgc	660
attatcataa	caattctgag	gatgtcctct	gccactggcc	gccagaaggc	atthttctact	720
tgttctcac	acctcattgt	ggtgtccctc	ttctacggaa	cagccagtct	gacctacctg	780
cggcccaaat	caaaccagtc	ccctgagagc	aagaagctag	tgtcattgtc	ctacactgtc	840

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900  
gtcaagagga caatcactca aaaagtctta cagaagttag atgtgttt 948

<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

atggcgaata gaaacaatgt gacagagttt attctattgg ggcttacaga gaatccaaaa	60
atgcagaaaa tcatatttgt tgtgttttct gtcactctaca tcaacgccat gataggaaat	120
gtgctcattg tggtcacat cactgccagc ccatcactga gatccccat gtactttttc	180
ctggcctatc tctcctttat tgatgcctgc tattcctctg tcaatacccc taagctgac	240
acagattcac tctatgaaaa caagactatc ttattcaatg gatgtatgac tcaagtcttt	300
ggagaacatt ttttcagagg tgttgaggtc atcctactta ctgtaatggc ctatgaccac	360
tatgtggcca tctgcaagcc cttgcaactat accaccatca tgaagcagca tgtttgtagc	420
ctgctagtgg gagtgtcatg ggtaggaggc tttcttcatg caaccataca gatcctcttc	480
actctgtcaat taccttttctg tggctccta atgcatagatc actttatgtg tgatctctac	540
actttgatca atcttgccctg cactaatacc cacactctag gactcttcat tgctgccaac	600
agtgggttca tatgcctgtt aaactgtctc ttgctcctgg tctcctgcgt ggtcactactg	660
tactccttaa agaccacacag cttagaggca aggcataag ccctctctac ctgtgtctcc	720
cacatcacag ttgtcatctt atcctttata ccctgcatat ttgtgtacat gagacctcca	780
gctactttac ccattgataa agcagttgct gtattctaca ctatgataac ttctatgtta	840
aaccctttaa tctacacctt gaggaatgct caaatgaaaa atgccattag gaaattgtgt	900
agtaggaaag ctatttcaag tgtcaaa	927

<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

tggaaaaatc atttcacctc tgtgaattgt ggttttgcca tctgcagagc tgaatgttaa	60
ccatagccca agatactaag tattatagga ttgaaatgaa atataaatga aactttgtaa	120
atgttaaatt ataacacaaa tcatatggtc agtgtcgatg tcctaattgt tcctaactcc	180
tcatcacact ctctacttc ttcatgttgg ctgccatcct gatatccgct ctgcagaggg	240
gaggcacaag gcttttccca cctgctcctt ccacctgggt taattctcct ccagcacaat	300
gaacaagcct cacctatttg tgccccagct ccactctctc ttatgagagg ggcaaggtag	360
tgtctacggg ttacacatgc atcactcctg tgccaaaccc cttgatctgc agcatgagga	420
agaaggaact caagcatgct cttaaaaaaa aagaagaaat tgcaagggtc ttgctgctca	480
gaacacat	488

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

atgttttagct ctgagccac catagatgga aatcagtccc tgtgtgccaa attcacattt	60
gtggcttttt cttctataga agaattacag cttgtactct tcatttgtgt cttaatcatc	120
acttatgcac tataggagga aatatcatca tcatctccct gatctggatc acccctgccc	180
tgcacactcc aatgtatttc ttctggtga acctctcatt tctggagatg tgctatacca	240



ccagtgtggt	gcctcatgct	ggtgcacctg	ctggtggaga	ccaaaacat	aagtgtgggt	300
ggctgtgcaa	cccagatgta	catatttgcc	atcttgggac	tgacagaatg	ctgcttgcta	360
gcagctatgg	cttacgatcg	ctttgtagct	atttgttacc	cactgcatta	cactctcttc	420
atgggccctc	gtgtttgttt	gaaattggct	gcagcatctt	ggttcactgg	agtgggtggtg	480
gagtcagccc	agatcacccct	gatcttcact	ttgcctttct	gtggaacagg	aaagattcaa	540
cacttttttg	tgacataatg	cctgtactga	aactggcttg	tattgatacc	tcccaaattg	600
aaattgtgat	gttttctctc	tccgtgctat	ttattgtgag	tccttgtttc	ctcattctgt	660
gctcccacat	gcacatccct	gtgaccatct	tgagaatccc	ttcagcagct	ggaagacaca	720
aagctttctc	cacttgttct	tctcatatct	tggttgtttc	tctgttctat	ggcactgcct	780
tgttcactta	cttgcaacct	aagactgcac	acactccaga	aacagacaaa	gcaactgcac	840
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&lt;210&gt; 1014

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g864 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1014

tccatgtacc	tggtcacgat	gctgaggaac	ctgttcatca	tcctggctgg	cagctctgac	60
ccccacttcc	acacccccat	gtacttcttc	ctctccaacc	tgctctgggc	tgacattggt	120
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tcttatgcgg	gctgcctgac	acagatgtct	ttctttgtcc	tttttgcatg	tatagaagac	240
atgctcctga	ctctgatggc	ctatgaccga	tttgtggcca	tctgcccac	tgacacccc	300
tgactaccg	agtcacatg	aatcctcacc	tctgtgtctt	cttagttttg	gtgtcctttt	360
tccttagcct	gttggaattcc	cagctgcaca	gctggattgt	gttacacaac	tcaccttctt	420
caagaatgtg	gaaatctata	atTTTTTTT	tgtgacccat	ctcaacttct	caaccttgcc	480
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ccatcgtcag	atgggaagta	taaagccttc	tccacctgtg	gctctcacct	ggcagttggt	660
tgcttatttt	atgaaacagg	cattggcgtg	tacctgactt	cagctgtgtc	atcatctccc	720
aggaatggag	tggtggcatc	agtgatgtac	gctgtgggtc	tcctcatgct	gaaccttttc	780
atctacagcc	tgagaaacag	ggacattcat	agtgcctgt	ggaggctgcg	cagcagaaca	840
gtcaaatctc	atgatctgtt	ccatcctttc	tct			873

&lt;210&gt; 1015

&lt;211&gt; 981

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g865 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1015

atggatgtct	ctatattcct	cctcctagaa	ccacagagga	tccagaacgg	cagccgggtcc	60
tcaactgggt	gttccctgtc	atgtgcctgg	tcacagtgtc	ggggaagctg	ctcatcatgt	120
tggccttcag	ccctgactcc	cacctccaca	cccacatgta	cttcttcttc	tccaacctgt	180
ccttgccctga	catcggtttc	acctccacca	ttgtcccca	gatgattgcg	gacatccagt	240
ctcacagcag	agtgatctcc	tatgcaggcc	gcctgactca	gatgtctctc	tttgccattt	300
ttggaggcat	ggaagacaga	catgtcctcg	agtgtgatgg	cctatgaccg	gtttgtagcc	360
atctgtcacc	ctctatatca	ttcagccatc	atgaatccgt	gtttctgtgg	cttccctact	420
ttgtttgtct	tttttttttc	tcagtctttt	agacacccag	ctgcacaact	tgattgcttt	480
acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	ttctgtgacc	cttctcaact	540
cccccatctt	gcattgtgtg	acaccttcac	caataacatc	atcgtgtatt	tcctgtctgt	600
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aaaaaaggca	gcaaggtcaa	a				981

&lt;210&gt; 1016

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g866 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1016

atgggtgaca	aggggaacagg	caaccattca	gatgtaactg	atttcattct	tgaaggcttc	60
agggtccgcc	cagagttcta	cattctcctc	ttcttctctg	tcctgctgat	ctatagcatg	120
gttcttttgg	ggaacattag	tgtgatgaca	atcattgtaa	ctgattccca	gctgaacaca	180
ccaatgtatt	tttttctagg	caacctctcc	ttcattgacg	tctcctactc	cactgttatt	240
gtcctctaaag	ccatggccca	cttctgtctc	gaaaaaaaga	cagtctcttt	tgcaggttgt	300
gttgcccagt	tattcctttt	tgccctgttc	attgtaacag	aggggtttgt	cctggcagcc	360
atggcctatg	accgcttcag	tgccatctgc	aatcctcttc	ttcatagtgt	tcacatgtca	420
agacgcctct	gcactcagtt	ggttgctggg	tcttatttct	gtggctgggc	cagttccatc	480
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&lt;210&gt; 1017

&lt;211&gt; 1008

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g867 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1017

tatacagacc	cacagaatct	aacagatgct	tcaaaatacc	tcctcctaga	actctcagag	60
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cagctgcaca	atttgattgc	cttacaatg	acctgcatca	aggatgtgga	aattccta	540
ttcttctgtg	acccttctca	actcccacac	cttgcggtgt	gtgacacctt	caccaataac	600
atagtcatgt	atttccttgc	tgccatattt	ggttttcttc	ctatctcacg	gatcattttc	660
tcttactata	aaattgtttc	ctccatgctg	agtgtttcat	catcaggtgg	gaagtataaa	720
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&lt;210&gt; 1018

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g868 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1018

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agcactctgg	ctgtcagctc	tgactgcccc	ctccacaccc	ccatgtactt	cttcctctcc	180
aacctgtgct	ggcctgacat	cggtttcacc	tcggccatgg	ttcccaagat	gattgtggac	240
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ctccttggtg	catgtataga	aggcatgctc	ctgactgtga	tgccctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
gttttgggtg	cctttttcct	tagcctgttg	gattcccagc	tgacagttg	gattgtgtta	480
caattaacca	tcatcaagaa	tgtggaaatc	tctaatttgg	tctgtgaccc	ctctcaactt	540
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gcagcagagc	attcgaatct	catgatctgt	tccatccttt	ttcttgtgt		949

&lt;210&gt; 1019

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g869 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1019

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ccaatgtatt	ttttcctagg	caatctctcc	ttcattgac	ttttctattc	atctgttatt	240
gaacccaagg	ctatgatcaa	cttctggtct	gaaaacaagt	ctatctcctt	tgcaggctgt	300
gtggcccagc	tctttctctt	tgccctcctc	attgtgactg	agggatttct	cctggcggcc	360
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acacgtctgt	gtactcagtt	ggtggctggt	tcctattttt	gtggctgcat	tagctcagtt	480
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ctagtcactc	ccatgttgaa	tccttttgatt	tactctctga	ggaacaaaga	tgtccaagag	900
gctctaaaaa	aatttctaga	gaagaaaaat	attattctt			939

&lt;210&gt; 1020

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g870 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1020

cattcttttc	tcagatatat	tttcgctaag	ttgacagggtg	agccagagct	tcaaccctct	60
ctctactctg	tgttttggtc	accctaactg	ggatgaccac	accacacctc	catgtaccca	120
ctgccacacc	tccatgtacc	tttatatctt	tagcttttcc	ttcatagggt	tcttctattc	180
ctctgtcatt	tctcccaaaa	tgacaataag	ctttgtgaca	gaaaagaaca	tcatcaccta	240
tgtgacatca	aacactcagc	cttttctctt	ggcttctttg	tcattagtga	ttactccata	300
ttatccacac	tggccttgga	tcactatgag	gccatgaccc	tgccggtctc	tttcataagt	360
ttcatttctg	tagatgggtc	ataagttata	gaatttgctg	atgctgtggt	ccatcaaggg	420

acatggacca	attcctgttt	tgtgatcaca	gttgcattgag	ccttaacttg	tgtaacatag	480
gcccgcctta	ggctgcctga	atcagtagct	atgtcagaag	caggtggatt	tgtattcatg	540
agaaccagca	gtgtaccatg	ctgtgttatc	attttcata	tttgttttca	ttcttttcaa	600
catttttcat	taaccacagt	gtccaaatct	tcagccagat	tccataaatc	tgttttattc	660
tttttttgg	ttagggacat	tcagttagct	cagatctcca	gaagctatgg	gttagtgtaa	720
attacagtgt	ccttcaccaa	gatggggcca	gtgatgaacg	gtctgttcaa	caccttgagg	780
aacaagacta	tctaacttgc	tgcaatgaaa	cctttgtcat	tttcttct		828

&lt;210&gt; 1021

&lt;211&gt; 1001

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g871 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1021

gatacagacc	cacagagtct	aacagatgtc	tctatatattcc	ttctcctcga	actctcagag	60
gatccagaac	tgtagccggg	cgtagctggg	ctgttcctgt	ccatgtgcct	ggtagcgggtg	120
ctggagaacc	tgtagcatcat	cctggccgtc	agccctgact	cccacctcca	caccccatgt	180
acttcttctc	ctccaacctg	tccttgccctg	acatcggttt	cacctccaca	cgggtcccaaa	240
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gatgtctctc	tttgccattt	ttggaggcag	ggaagagaga	catgctcctg	agtgtgatgg	360
cctacgacca	gtttgtagcc	atctgtcacc	ctccatatcg	ttcagccatc	ttgaacctcg	420
gtttctgtgg	cttcttagat	ttgttgctct	tggttttttt	tttttttttt	ttttttccct	480
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ttccttttgt	aggatgggtt	aaaaaaggca	gcaagggtcaa	a		1001

&lt;210&gt; 1022

&lt;211&gt; 1025

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g872 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1022

gatacagacc	cacagagtct	aacagatgtc	tctatatattcc	ttctcctcga	actctcagag	60
gatccagaac	tgtagccggg	cgtagctggg	ctgttcctgt	ccatgtgcct	ggtagcgggtg	120
ctggggaacc	tgtagcatcat	cctggccgtc	agccctgact	cccacctccc	caccccatgt	180
tacttcttcc	tctccaacct	gtccttgccct	gacatcggtt	tcacctccac	cacgggtcccc	240
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gcctatgacc	tgtttgtacc	catctgtcac	cttctatatc	gttcaaccat	cttgaacctcg	420
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gcctgagaaa	cggggatatt	aaaagtgtcc	tacggcggcc	gcattggcagc	acagtctaat	960
ctcaatacgt	tcttatctgt	tccattcctt	ttgtagggtg	ggtaacaaa	gacagcaagg	1020

tcaaaa

1025

&lt;210&gt; 1023

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g873 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1023

atggatctgg	ggaactcagg	gaatgattca	gttgtgacca	agtttgtcct	gctgggcctc	60
acagagactg	cagctctaca	gcccacctc	tttgtcatct	tccttcttgc	ttacgtcact	120
accattggag	gcaccctcag	catcctggcg	gccatcctta	tggaaaccaa	actccacagc	180
cccatgtact	tcttcttggg	gaacttgtcc	ctgccagatg	tgggggtgtg	cagtgtcact	240
gtccctgcca	tgctgagcca	tttcatatcc	aacgacagaa	gcattcccta	taaggcctgc	300
ctctccgagc	tcttcttctt	ccacctcctg	gctggggcag	actgcttctt	gctgaccatc	360
atggcctatg	accgctatct	ggccatctgc	cagtcacctca	cctacagcag	ccgcatgagc	420
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ttgctgtttg	tagcagcagc	tttcatgggt	gtggccccct	tggctctcat	cactgtgtcc	660
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tcacctctta	atagccatgg	ccta				1044

&lt;210&gt; 1024

&lt;211&gt; 688

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g874 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1024

atgtctatac	ctagctccac	caggaaaatg	gcagcagaaa	gtcactctac	ggtgacagag	60
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aaaaccgtag	tggggggcct	catcttgatc	actctagttt	tccttaattc	tcagcttcac	180
cctcccatgt	actacgtcat	cagaaattta	tcatttatgg	atcactgcaa	ttgctctatt	240
agtaccccta	aaatactggg	gaagtttgtg	ttagagaaga	ccatcatctc	ctatgaggac	300
ggcatgtcac	agctttgtag	tgcttcgtgt	ttatatgttc	atggccaagc	gtaacatgag	360
gaccagcaac	tgctgtcatc	acatttcac	aagtcagctc	cctgctggta	gttgtagtat	420
ttatatggag	ttgactggta	caacaataga	tattttgcct	tgtattaaaa	tagtactagt	480
gtgagttatt	catcagtcac	acttctctca	tgcactagca	tctatgatat	tgataggaca	540
atcttctttt	ttacttgatg	caatattgta	gtcactagat	taacagttgt	ttcctactcc	600
ttttctctcc	agcatcctcc	acatcagctt	tacaaagggc	aagctctggg	tttttcccgt	660
aggtctgacg	cattcatgct	gttgcctt				688

&lt;210&gt; 1025

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g875 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1025

cacacagagc	cacggaatct	cacaagtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccgct	cctcgctttg	ctgtccctgt	ccctgtccat	gcattctggc	120
atgggtgctga	ggaacctgct	caacatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccacgtact	tcttctcttc	caacctgtgc	tgggctgaca	tcggtttcac	ctcggccacg	240
gttcccaata	tgattgtgga	catgcagtcg	catagcagag	tcatctctca	tgcggactgc	300
ctgacacaga	tttctttctt	gtctcttttt	gcattgtatag	aaggcatgct	cctgactgtg	360
atgacctatg	actgctttgt	agccatctgt	tgccctctgc	actaccagct	catcgtgaat	420
cctcacctct	gtgtcttctt	cgttttgggtg	tcctttttcc	ttagcctgtt	ggattcccag	480
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gtctgtgacc	cctctcaact	tctcaaaactt	gcttgtttctg	acagcgtcat	caatagcata	600
ttcatgcatt	tccataatac	tatgtttgggt	tttcttccca	tttcagggat	ccttgtgtct	660
tactataaaa	tgttcccttc	cattcttagg	atttcatcgt	cagatgggaa	gtataaaagcc	720
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tacgtgtggg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	caggacata	900
caaagtgcc	tgtggaggct	gtcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttcttggg	tgggtaaggg	caaccacatt	aaa			993

&lt;210&gt; 1026

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g876 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1026

cacagagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccgct	ctcgctttgc	tgtccctgtc	cctgtccatg	tatctgggtca	120
cgggtgctgag	gaacctgtc	agcatcctgg	ctgtccgctc	tgactcccc	ctccacaccc	180
ccatatactt	cttctctctc	aacctgtgct	gggctgacat	cggtttcacc	tcggccacag	240
ttcccaagat	gattgtggac	atgcagtcgc	atagcagagt	catctctcat	gcaggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgcttttga	gccatctgtc	accctctgca	ctaccagctc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttgggtg	ccttttttcc	ttagcctgtt	gattcccagc	480
tgcacagttg	gattgtgtta	caattcacca	tcattcaaga	tgtggaaatc	tctaattttg	540
tctgtgacct	ctctcaactt	ctcaaatttg	cctgttctga	cagcatcatc	aatagcatat	600
tcataatatt	ccatagtact	atgtttgggt	ttcttcccat	ttcagggatc	cttttgtctt	660
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acgctgtggg	cacccccatg	ttgaaccttt	tcattctacag	cctgagaaac	aggacatac	900
aaagtgcctt	gtgggggctg	cacagcagaa	cagtcgaatc	tcattgatctg	ttccatcctt	960
tttct						993

&lt;210&gt; 1027

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g877 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1027

atgcagccag	aatctggggc	caatggaaca	gtcattgctg	agttcaccct	gctgggcttg	60
ctggaggcgc	cagggtctga	gccagttgtc	tttgtgctct	tcctctttgc	ctacctgggc	120
acggctcagg	gcaacctcag	catcctggca	gctgtcttgg	tggagcccaa	actccacacc	180
cccattgtact	tcttctctgg	gaacctatca	gtgctggatg	ttgggtgcat	cagcgtcact	240
gttccatcaa	tgttgagtcg	tctcctgtcc	cgaagcgtg	cagttccctg	tggggcctgc	300
cttaccacag	tcttcttctt	ccatctgttc	gttggagtgg	actgcttctt	gctgaccgcc	360
atggcctatg	accaattcct	ggccatctgc	cggccctcca	cctacagcac	ccgcatgagt	420

cagacagtcc	agaggatggt	ggtaggctgcg	tcctgggctt	gtgctttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgtgat	caatcacttc	540
tactgtgacc	ccccacagct	cttccagctc	tcctgtccca	gcacccaact	caatgagctg	600
ctgctttttg	ctgtgggttt	tataatggca	ggtagcccca	tggctctcat	tgatcatctc	660
tatatccacg	tggcagctgc	agtcctgcga	attcgctctg	tagagggcag	gaagaaagcc	720
ttctccacat	gtggctccca	cctcactgtg	gttgccatat	tctatgggtt	aggatatctt	780
aactatatgc	gactgggttc	aaccaagctt	tcagacaagg	ataaagctgt	tggaaatttc	840
aacactgtca	tcaatcccat	gctgaacca	atcatctaca	gcttcagaaa	ccctgatgtg	900
cagagtgcga	tctggaggat	gctcacagg	aggcggtcac	tggt		945

&lt;210&gt; 1028

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g878 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1028

atgacagatt	acaatgaacc	aatggaacca	atggaagata	agaaccagac	agtagtgact	60
gaatttctct	tattgggect	cacagatcat	ccctatcaga	agattgttct	cttcttcatg	120
tttctctttg	tttatcttat	caccctggga	ggtaacttgg	ggatgatcac	tctcatatgg	180
attgatccca	gactccacac	tcctatgtac	ttttttctta	ggcacttgtc	ctttgtagat	240
atttgttctt	cttcttctgt	tgtgcctaag	atgctgtgta	atatctttgc	agagaaaaaa	300
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gagtgttttc	tcctggctgc	catggcatat	gaccggtagt	tggccatctg	caagcccttg	420
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ggtctgatca	tcattggtctc	ctatatttgc	atcctgatga	ccatcttgaa	gatccagact	720
gctgatggga	agcaaaaagc	tttcttcacc	tgtttttctc	accttgccgc	tgtctccatc	780
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tataaagtga	tttctctatt	ttatactgtg	gtaatcccca	tggttaaccc	ccttatctac	900
agcttgagga	ataaggaggt	gaaagatgca	ttcagaagaa	aaattgagag	gaaaaaattt	960
attataggt						969

&lt;210&gt; 1029

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g879 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1029

ttcttttctt	tagacctcat	tagaagccaa	gcaaatacaa	tgtcaaagaa	acactggaca	60
gccatagctg	agttttattcc	cctgggaccg	acagatcaag	ccgagttgca	gcttgtcctt	120
tttttctgtc	acgttccctgg	tcattttacct	tattatggta	atgggcaatt	tgagcatgat	180
tttgatcatt	agaagtgact	gaaaacttca	cattccaatg	tacttcttcc	tcagtcacct	240
ctccttttga	gttctctgtt	atactctcaa	tgtcactcct	cagatattgg	ttaatttctt	300
atccaagaga	aaaaccattt	tcttcattgg	ttgtgtaagt	gtttttataat	tctacttttt	360
cattgtcctg	ataatcacag	attatcatat	gcttacagtg	atgggctaag	actgctacat	420
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tcttctgtcc	ttctgaggat	ccaatgagat	caaccacttt	gactgtgcgg	acccccctct	600
gttagtcctc	ccttgccgag	gtacctgtgt	caaataaatc	atcatgttga	tggagccaca	660
ctgtcttttg	aaacctggat	atatttt				687

&lt;210&gt; 1030

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g880 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1030

atgtatctgg	tcacgggtgct	gaggaacctg	ctcagcatcc	tggctgtcag	ctctgactcc	60
cacccccaca	cacccatgta	cttcttcctc	tccaacctgt	gctgggctga	catcggtttc	120
accttggcca	cggttcccaa	gatgattgtg	gacatggggg	cgcatagcag	agtcattctt	180
tatgggggct	gcctgacaca	gatgtctttc	ttgggtactt	ttgcatgtat	agtagacatg	240
ttcctgactg	tgatggctta	tgactgcttt	gtagccatct	gtcgccctct	gcactaccca	300
gtcatcgtga	atcctcacct	ctgtgtcttc	ttcggttttg	tgcccttttt	ccttagcctg	360
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atcaatagca	tattcatata	ttttgataat	actatgtttg	gtttctctcc	catttcaggg	540
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aaacagggac	attcaaagtg	ccctgtggag	ggtgtgcaac	aaaacagtcg	aatctcatga	840
tctgttccat	cctttttct					859

&lt;210&gt; 1031

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g881 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1031

atggctaatt	aaaactacac	aaaggtcacc	taattcattt	tcacaggctt	gaattacaat	60
cctcagttgc	gggtcttcct	tttcctactc	tttctgacaa	ctttctatgt	catcaatgta	120
actggaaact	tgggaatgat	gtccctcatc	cgaattgatt	cccgccttca	cacacccatg	180
tactttttcc	tcagccacct	gtcctttgtg	gacacctgct	tctcctcagt	tgtgagcccc	240
aagatgctca	ctgacttctt	tgtgaagagg	aaagccattt	ctttccttgg	ctgtgctttg	300
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gcagtgatcc	ctatgttgaa	cccacttatc	tacagcttga	gaaacaagga	agtcaaagat	900
gccatccaca	ggactgtcac	tcagaggaag	ttttgcaagg	cctaaattct	tatccagaag	960
gaattagggg	ggaaa					975

&lt;210&gt; 1032

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g882 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1032

atggagactg	aaaacaatac	aacagtgaca	gagttcatta	ttttgggatt	aacagacaat	60
cctatgctat	gtgccatttt	cttcgtgttt	tttctagcag	tttatatagt	tactataccg	120



ggaaatatta	gcataatcct	cttaatccaa	agcagccac	agcttcacac	gctaattgtac	180
ctttttctca	gccatttggc	ttctgtggac	attgggtatt	ccatatcagt	tacgccaatc	240
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cttggtctcg	atgtcatgtt	tggaaaccaca	gagtgtcttc	tgctgggtcac	tatgtggcta	360
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tccttatcag	cacgtgtttt	accataatcg	tgctctacat	ctacatcctt	cactccatcc	660
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acccctcat	ctacagtctc	aggaataagg	agggtgaaaga	ggccatgaga	aaattgatgg	900
caagaacaca	ttggttttcc	tgaattaaat	cagtataatc	c		941

&lt;210&gt; 1033

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g883 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1033

atctttgcca	tcttgaccac	cattgactgc	tgtgtatttg	tctgggaatt	cctggagtgc	60
acagtctttg	tgaataagag	ggcatgtgc	cagctggcgt	gtgggtgcctt	ttgcattggc	120
ctgatcatga	cagtggctca	aataaccaca	gtgtcacaga	ggtacaaaag	gagcacatat	180
gctattttaga	ctgcttcttg	tttgacaccc	ttcttgtcat	gaaactctcc	tgcattgaca	240
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tgtctgtgct	tgtactgctt	acctcaagca	caagccaatg	aattcaatag	aaaacaggtc	480
ttctataaga	gacctacatt	atcatcatte	attctgcctc	tggacactgt	tgtttacact	540
ctgaggtaca	tggaggccaa	ggataccatg	tacagagctg	tggacagaaa	tatttcttaa	600
cagatt						606

&lt;210&gt; 1034

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g884 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1034

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtctc	tcctctttgc	ctatctggtc	120
acaactgggg	gcaacctcag	catcctggca	gccgtcttgg	tggagcccaa	actccacgcc	180
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tacagccacg	tggcagctgc	agttctacga	atccgttcag	tggaggggccg	aaagaaggcc	720
ttctccacgt	gtggctccca	cctcaccgtg	gtttgtcttt	tctttggaag	aggtatcttc	780
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aacactgtta	tcaaccctat	gctgaacctt	cttatctaca	gcctcagaaa	ccctgatggt	900
caggggtgctc	tgtggcaaat	atttttgggg	aggagatcac	tgacc		945

<210> 1035  
 <211> 927  
 <212> DNA  
 <213> Unknown (H38g885 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1035  
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 ggaaagcatc agataaccct ctttgtgggt ttcctaactg tctacatttt aactctgggt 120  
 gctaacatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180  
 ttcttctctaa gcatgctggc tagttcagag acgggtgtaca cactgggtcat tgtgccacga 240  
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300  
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat 360  
 gaccgctatg tggccatctg cagaccctg agatacactg tcatcatgag caaggggacta 420  
 tgtgcccagc tgggtgtgtg gtcctttggc attggtctga ctatggcagt tctccatgtg 480  
 acagccatgt tcaatttggc gttctgtggc acagtggtag accacttctt ttgtgacatt 540  
 taccagtc tgaactttc ttgcattgat accactatca atgagataat aaattatggg 600  
 gtaagttcat ttgtgatatt tgtgcccata ggcctgatat ttatctccta tgtccttgct 660  
 atctcttcca tccttcaaat tgccctcagc gagggccgga agaagacctt tgccacctgt 720  
 gtctcccacc tcaactgtgt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780  
 ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgtacgta caccatcatc 840  
 actcccttgc tgaacctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta 900  
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036  
 <211> 958  
 <212> DNA  
 <213> Unknown (H38g886 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1036  
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 ctcttgaggga tctcagagag tcctgagcag cagcagatgc tgttttggat gttcctgggtc 120  
 aggtacctgg tcacggtgct gggaaatgtg ctcatcatcc tggccatcag ctctgattcc 180  
 cgctgcaca ccccatgta cttcttctct gccaacctct ccttcaactga cctcttcttt 240  
 gtcaccaaca caatcccaa gatgctgggt aacctccagt cccagaacaa agccatctcc 300  
 tacacagggt gtctgacaca gctctacttc ctggtctcct tgggtggccct ggacaacctc 360  
 aacctggcgg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccaactatgtc 420  
 acagccatga tccctgggct ctgtatcttg ctctctcct tgtgttgggt gttctctgcc 480  
 ctctatggcc tcatccatat cctcctcatg accaggtgac cttctgtggg tctcaaaaga 540  
 tccactacct cttctgtgag atgtacttcc tgctaaggct ggcatgttcc aacatccacg 600  
 tcaaccacac agtactggtt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660  
 tgatcacatc ctacgccgc attgtcagag ccacctcca aataccctca gccactggga 720  
 agtaaaaagc cttctccacc tgtgcttccc atttggtgtg ggtctccctc ttctatggga 780  
 ctctgggtat ggtgtacctg cagcccctcc aaacctactc catgaaggac tcagtagcca 840  
 cagtgtgta tgcggtggtg acgcatgat taacctttc atctacagcc tgaggaacaa 900  
 ggacatgcat ggggctctgg gaagacttcg ccaaggaaaa gccttccaga agttgaca 958

<210> 1037  
 <211> 828  
 <212> DNA  
 <213> Unknown (H38g887 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1037

atgcgaagaa	agaacctcac	agaggtaaca	gagtttgttt	tcctggggatt	ctccagattc	60
cacaaacatc	acatcactct	ctttgtgggt	tttctcatcc	tgtacacatt	aactgtggct	120
ggcaatgcc	tcatcatgac	catcatctgc	attgaccgtc	acctccacac	tcccatgtac	180
ttcttctga	gcatgctggc	tagctcaaag	acagtgtaca	cactgttcat	cattccacag	240
atgctctcca	gcttcgtaac	ccagaccag	ccaatctccc	tagccggttg	taccacccaa	300
acgttcttct	ttgttacctt	ggccatcaac	aattgcttct	tgctcacagt	gatgggctat	360
gaccactata	tggccatctg	caatcccttg	agatacagg	tcattacgag	caagaagggtg	420
tgtgtccagc	tgggtgtgtg	agccttttag	attggccttg	ccatggcagc	tgtccaggta	480
acatccatat	ttaccttacc	tttttgtcac	acggtgggtg	gtcatttctt	ctgtgacatc	540
ctccctgtca	tgaacctctc	ctgtattaat	accactatca	atgagataat	caattttgtt	600
gtcagggtat	ttgtcatcct	ggccccatg	ggtctgggtc	tcattctccta	tgtcctcatc	660
atctccactg	tcctcaagat	tgcctcagct	gagggttgg	agaagacctt	tgccacctgt	720
gccttcacc	tcactgtggt	cattgtccat	tatggctgtg	cttccattgc	ctacctcatg	780
cccaagtcag	aaaactctat	agaacaagac	ctccttctct	cagtgacc		828

&lt;210&gt; 1038

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g888 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1038

atggatggag	ataaccagag	tgagaactca	cagttccttc	tcctggggat	ctcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggt	cacgggtgctg	120
ggaaatgtgc	tcatcatcct	ggccatcagc	tctgattccc	acctgcacac	ccccatgtac	180
ttcttcctgg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaag	240
atgctggtga	acttccagtc	ccagaacaaa	gccatctcct	atgcagggtg	tctgacacag	300
ctctacttcc	tggctctcct	ggtgaccttg	gacaacctca	tcctggccgt	gatggcgat	360
gatcgctatg	tggccatctg	ctgccccctc	cactatgtca	cagccatgag	ccctgggctc	420
tgtgtcttgc	tcctctcctt	gtgttggggg	ctgtctgttc	tctatggcct	cctcctcacc	480
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atgtacatcc	tgtctgtggt	ggcatgttcc	aacaccacac	tcattcacac	agcattgatt	600
gccactggct	gcttcatctt	cctcaccctc	ttagggttca	tgaccacatc	ctatgtacgt	660
attgtcagaa	ccatccttca	aatgccctcg	gcctctaaga	aatacaaaac	tttctctacc	720
tgtgcctcgc	atttgggtgt	ggtctccctc	ttttatggga	cgcttgctat	ggtgtacctg	780
cagccctcc	atacctactc	catgaaggac	tcagtagcca	cagtgatgta	tgtgtgctg	840
acacctatga	tgaacctttt	catctacagc	ctgaggaaca	aagacatgca	tggggctccg	900
ggaagagtcc	tatggagacc	ctttcagagg	cctaaa			936

&lt;210&gt; 1039

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g889 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1039

atggctgatg	gaaatataaa	aggatcacag	aattcatttt	tgtaggctta	aggtatcatc	60
ttcagctgca	agtcttctt	ttcttaccat	ttctaccttt	ttacctcat	tactatgaca	120
gaaaacttgg	gcatgatggt	tcgcatctgg	ctcgattcct	gctttcacac	acctatgtac	180
tttgtctca	gctacctgtc	ctttgtggac	atctgcttct	catccgttgt	gggccacaag	240
ttgtcactg	acttatttgc	tgtaaggaaa	gccatctctt	tcctgggctg	tccttgcag	300
cagtggttct	ttgggttctt	cgtagtcat	gagtatcttc	tcttggcttc	catggcctat	360
gacaattatg	tggccatctg	taaccatttg	ttgtactcag	tggccatgta	atagagactg	420
tgcattcagc	tgggtgtgtg	acgttatgca	gctgatttct	tcaacacat	aactcacaca	480
acggctgctt	ttcattttcc	cttttttcc	tccaacatta	tcaatcattt	cttctgtgac	540
atgtctctcc	ttctttctct	cgtgtgtgct	gacgcccgga	tcaataaatt	gttagttttc	600

attgtggctg	gagctgtact	agttgtcagt	agcctgacca	ttataatctc	ctatTTTTtac	660
atccttactg	acattctgag	gatctgctct	gctaattggg	aagaacaaaa	ctTTTTccac	720
ctgctcttca	cacttaacag	ctgtttccat	cttttatggg	tctctcttct	ttagctacgt	780
ttcgaccagg	tgcaactttt	taccggaac	tcaataaaat	agtgttggtg	ttctgtacat	840
ccccatgttg	aaacctctca	tctacagctt	gataaataaa	gaagtatcct	agccacta	898

&lt;210&gt; 1040

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g890 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1040

atggaaaaaa	taaacaacgt	aactgaattc	atTTTctggg	gtctTTTctca	gagcccagag	60
attgagaaag	tttgttttgt	ggtgttttct	ttcttctaca	taatcattct	tctgggaaat	120
ctcctcatca	tgctgacagt	ttgcctgagc	aacctgttta	agtcacccat	gtatttcttt	180
ctcagcttct	tgtcttttgt	ggacatttgt	tactcttcag	tcacagctcc	caagatgatt	240
gttgacctgt	tagcaaagga	caaaacctac	tcctatgtgg	ggtgcatgtt	gcaactgctt	300
ggagtacatt	tctttgggtg	cactgagatc	ttcatcctta	ctgtaatggc	ctatgatcgt	360
tatgtggcta	tctgtaaacc	cctacattat	atgaccatca	tgaaccggga	gacatgcaat	420
aaaaagttaa	tagggacgtg	ggtaggtggg	ttcttacact	ccattatcca	agtggctctg	480
gtagtccaac	tacccttttg	tggacccaat	gagatagatc	actacttttg	tgatgttcac	540
cctgtgttga	aacttgccctg	cacagaaaca	tacattgttg	gtgttgttgt	gacagccaac	600
agtggtagca	ttgctctggg	gagtttttgt	atcttgctaa	tctcctacag	catcatccta	660
gtttccctga	gaaagcagtc	agcagaaggc	aggcgcaaaag	ccctctccac	ctgtggctcc	720
cacattgcca	tggctcgttat	ctttttcgag	cccctgtact	tttatgtaca	tgcgccctga	780
tacgaccttt	tcagaggata	agatgggtggc	tgtattttac	accattatca	ctcccatggt	840
aaatcctctg	atttatacac	tgagaaatgc	agaagtaaaag	aatgcaatga	agaaactgtg	900
gggcagaaat	gttttcttgg	aggctaaagg	gaaa			934

&lt;210&gt; 1041

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g891 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1041

atggactata	gaaatcaaac	tttggttact	gaattTTTTt	ccgtggggatt	aacaaatctc	60
tttcagcaca	agattgctct	ctttctggta	tttctctttg	tttatcttgt	cactgttccg	120
ggaaacttgg	gaatgatcac	tcttattttg	atggattctc	gactccagac	ccccaagtac	180
ttttctctct	gccacttgct	ctttgtggat	gtctgctcct	cttctgccat	cgggtcccaag	240
atgttgactg	atatcttcgt	ggagaaaaaa	gtaatctctt	tgggtgtgtt	gcccagttat	300
ggttttttgg	ccatttttga	gtaactgaat	gtttccttct	ggctgccatg	gcatatgacc	360
ggtataggct	atctataagc	ctttgttgtg	tacactcatt	atgtcccaac	aggtctgtgt	420
gcagctgggt	gtgggcctta	tgctgtgggc	cttataagca	ccatgacca	tatgactttc	480
acctttcgcc	tactctactg	tggtccaaac	atcatcaatc	acttcttctg	tgaccttctc	540
cctgtcctct	ccctggcata	tgagataacc	catattaata	aatgtttact	ttttatcttg	600
gtgggtgccc	tgggagtact	cagtgggtgtg	atcatcttgg	tctcctacat	ttacattgtc	660
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tcacacctga	tggctgtctc	catcctgtat	gggacactct	tctttatctg	tgtatgtcca	780
agctctagtt	tctctatcaa	catcaataaa	gtgggttccc	tgttctacac	agcagtgatc	840
cccatgttga	atcccccttat	ctacagcctg	agaaacaagg	aggtaaaaga	ttcattcagc	900
aagaagtttg	aaagaaagaa	gtttcttata	ggtaggtgaa	ctagaatacc	a	951

&lt;210&gt; 1042

&lt;211&gt; 930

&lt;212&gt; DNA

<213> Unknown (H38g892 nucleotide)

<220>

<223> Synthetic construct

<400> 1042

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atgcaggcta	tgctatttct	gatttttctg	atcctgtatg	gcatagctgt	gggtgggaaac	120
cttggcatga	ttgtaattat	ctgggtagat	gcacacctcc	acacccaat	gtatgccttc	180
ctgcaaagcc	tttcattgtt	ggacatctgc	tattcctcca	caattgcacc	cagggtctctg	240
gcgaactcca	tgcaagagga	ccacacaatt	tcctttggcg	gatgtgctgc	tcagttcttt	300
ttcttgtctc	tcctttggat	cacagaggct	ttcctcctgg	ctgccatggc	ctatgaccgc	360
ttcatcgcca	tctgcaaccc	tcttctgtac	tctgtgagca	tgtctcacca	ggctctgtgtg	420
ctgttaatat	caggatccta	cttgtggggg	gtagtcaatg	ccattgctca	aacaacctatg	480
accttcaggt	tgcttttctg	tgggtccaat	gagatcaacg	actttttctg	tgatgttccc	540
ccactcttgt	ccctctcatg	ttcagatacc	tttataaacc	aactgggttct	tccttggttta	600
tgtggctcca	ttattgtcag	tacctttttg	attgtcctgg	tctcatacat	ttacatcatc	660
tcaacaattc	tgaggatccc	gaccatgcag	ggacgctaga	aagccttctc	cacgtgcgct	720
tcccacctaa	caggagtgtg	cttgtttttt	ggtagctgtt	tcctcatgta	tgcacaaccc	780
agtgccatct	tcctcatgga	gcaaagtaaa	atagtgtcca	tattctacac	tatggctcatc	840
cccattgctga	atcccctgat	atacagcctg	aggaacaaag	aggtcaagca	ggctctgaga	900
cggagcatgc	agaagctgtc	tttgtgatca				930

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

atgagggaaa	ataaccagtc	ctctacactg	gaattcatcc	tcctgggagt	tactgggtcag	60
caggaaacagg	aagatttctt	ctacatcctc	ttcctgttca	tttaccocat	cacattgatt	120
ggaaacctgc	tcattgtcct	agccatttgc	tctgatgttc	gccttcacaa	ccccatgtat	180
tttctccttg	ccaacctctc	cttgggtgac	atcttcttct	catcggtaac	catccctaag	240
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atgtatttca	tgatagcctt	gggtaacaca	gacagctata	ttttggctgc	aatggcatat	360
gatcgagctg	tgcccatcag	ccaccactt	cactacacaa	caattatgag	tccacggtct	420
tgtatctggc	ttattgtctg	gtcttgggtg	attggaaaatg	ccaatgccct	ccccacact	480
ctgctcacag	ctagtctgtc	cttctgtggc	aaccaggaag	tggccaactt	ctactgtgac	540
attacccctt	tgctgaagtt	atcctgttct	gacatccact	ttcatgtgaa	gatgatgtac	600
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ttctccacag	tcctccaggt	tccttcacc	aagggcgtgc	tcaaggcctt	ctccacctgt	720
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cctttgacca	attatagcct	aaaagacgca	gtgatcactg	taatgtacac	ggcagtgacc	840
ccaatgttaa	atcctttcat	ctacagtctg	agaaatcggg	acatgaaggc	tgccctgcgg	900
aaactcttca	acaagagaat	ctcctcg				927

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

atgaagaaaag	aaaatcaatc	ctttaacctg	gattttattc	tcctgggagt	tactagtcag	60
caagaacaga	ataatgtctt	ctttgtgatt	tttttgtgca	tttaccocat	cacactgact	120
ggaaatctgc	tcattcatctt	ggccatctgt	gctgacattc	gccttcacaa	ccccatgtat	180

tttctccttg	ccaacctctc	cttggttgac	atcatcttct	catccgtaac	catccctaag	240
gtgctggcca	accatctctt	gggcagcaag	tcatctctct	ttgggggatg	cctaattgcag	300
atgtatttca	tgatagcctt	ggccaaggca	gacagctata	ccttggtctg	aatggcatac	360
gatcgagctg	tggccatcag	ctgcccactt	cattacacaa	caattatgag	tccacggtct	420
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attatgcctt	tgtgaagtt	gtctgttctt	gacgtccact	ttaatgtgaa	gatgatgtac	600
ctagggtcg	gcgttttctc	tttgccatta	ctatgcatca	ttgtctccta	tggtcaggtc	660
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ggctcccacc	tcacagttgt	ttttttatat	tatggtacaa	cgatgggcat	gtatttccgc	780
cctctgacca	gttacagccc	caaagatgca	gtgataactg	tgatgtatgt	ggcagtgacc	840
ccagcattaa	atcctttcat	ctatagtctg	agaaattggg	atatgaaggc	agccctacag	900
aaactcttca	gcaagagaat	ctcctca				927

&lt;210&gt; 1045

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g895 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1045

gctcttcttt	tccatttcta	caaacatccc	acccagagga	gaatgactgt	caaaagtcac	60
tctatagtga	cagagttcag	tctcagggga	ttaacgaagc	agccagatct	ccagctcttt	120
cacttcttca	ttttccttga	tatccatatg	gtcacaatgg	tggggaactt	gggcatgatc	180
actctaattt	gtcttaactc	tcagcttcac	acccccatgt	actacttctt	cagcaatctg	240
tcactcttgg	atctctgcta	ttcctccatt	actaacccta	agatgctggt	gaactttgtg	300
ttaaagaaga	gcattatctc	ttatgcaggg	tacatgtcat	agttctactt	tttctggtt	360
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ccctattgtg	aactcctcac	cagtcgctgc	ttctgtgaca	tcctccctct	catgaaactc	600
tctgatcta	gtgccttatg	atgttgagat	ggcagtcctc	ttttttgcta	gattgcaacc	660
tgagaatcat	gatcttaaca	gttcttgttt	tcttacacct	tcattctctt	cagcatectg	720
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cccctaattg	acagcctgaa	aaacaaggat	gtaaaagctg	ccatgcagaa	aacactaagg	960
agtaagtttt	gttgcagatg	taattatctt				990

&lt;210&gt; 1046

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g896 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1046

ctcctggaag	gagggaatca	gactagcacc	tttgagttcc	tcctctgggg	actctcagac	60
cagccacagc	agcaacacat	cttcttccctg	ctgtttctgt	ggatgtacgt	ggtcactgtg	120
gctgggaacc	tgctcattgt	cctggccatt	ggcactgaca	cacacctcca	cacctctatg	180
tacttcttcc	ttgccagctt	gtcgtgtgca	gatatctttt	ccacctccac	cactgtgccc	240
aaggccctgg	tgaatatcca	gacctagagc	aggctccattt	cctacgcagg	gtgtttggca	300
cagctctact	tcttcttgac	ttttggggac	atggacatct	ttctcccggc	tacaatggcc	360
tatgaccgct	atgtggccat	ttgccacctg	ctccactata	tgatgatcat	gagcctccac	420
cgctgtgcct	tcctggtgac	agcctgtctg	acctcaciaa	gtcttctcgc	catgactcgc	480
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acagtgggtga	ctccccgtct	gaaccccttt	atttacagca	tgcggaacaa	ggacatgaag	900
gcggcggttg	ttagacttct	caagggcagg	gtctccttct	cacagggc		948

&lt;210&gt; 1047

&lt;211&gt; 1007

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g897 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1047

gatacagacc	cacagagtct	aacagatgtc	tctatatattcc	tcctcctcaa	actctcagag	60
gatacagaac	tgcagcaggt	cgtcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tactcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttgttcc	tctccaacct	gtcccttgcc	tgacatcggt	ttcacctcca	ccacggtccc	240
caagatgatt	gtggacatcc	agtctcacag	cagagtcac	tcctatgcag	gctgcctgac	300
tcagatgtct	ctctttgcca	tttttgagg	tatggaagag	agacatgctc	ctgagtgtga	360
tggcctatga	ccggtttgta	gccatctgtc	accctctata	ttgttcagcc	atctttaacc	420
cgtgtttctg	tggcttcccta	gatttgttgt	cttttttttt	ttttttctca	gtctttcaga	480
ctcccagctg	cacaacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaattcc	540
taattttctc	tgggaacctt	ctcaactctc	ccatcttgca	tgttgtagaca	ccttcaccag	600
gaacatcagt	atttcctctg	tgccatattt	ggttttcttc	ccatcttggg	gacccttttc	660
tcttactgta	aaattgtttc	ctccattctg	agggtttcat	catcagggtg	gaagtataaa	720
ccttctccac	ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcattg	780
gagggtacct	cggttcagat	gtgtcatctt	ccccgagaaa	gggtgcagtg	gcctcagtg	840
tgtacatgg	ggtcaccccc	atgctgaacc	ccttcatcta	cagcctgaga	aacagggata	900
tgaaaagtgt	cctgcggcgg	ccgcatggca	gcacagtcta	atctcaacat	cttcttatct	960
gttccattcc	ttttgtaggg	tggtttaaaa	aaggcgccaa	ggcctaaa		1007

&lt;210&gt; 1048

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g898 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1048

atgagacaga	ataataatat	tacagaat	gtcctcctgg	gcttctctca	ggatctggat	60
gtgcaaaaag	cattatttgt	catattttta	ctcacatact	tggtgacagt	ggtggggaac	120
ctgctcattg	tgggtgactat	tattaccagc	ccttccttgg	gctccccaat	gtacttcttc	180
cttgctgccc	tgtcatttat	agatgctgca	tattccacta	caatttctcc	caaattgatt	240
gtagacttac	tctgtgataa	aaagactatt	tctttcccag	cttgcatggg	ccagttattt	300
ataaccact	tgtttgggtg	ttctgaggtc	ttccttcttg	tggtgatggc	ctgtgatcac	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgaaatc	420
cttctgttgg	tgggtggtcgt	gactggaggt	tttctgcatt	ctgtgtttca	aattgttgtt	480
gtatacagtc	tcgctttctg	tggccccaat	gtcattgact	actttgtctg	tgacatgtac	540
ccattattgg	aactgggtatg	actgcacacc	tactttattg	gccttactgt	ttttgtcaat	600
ggtggaacaa	tctgtatagt	cgtcttcacc	ctctactata	tctcctatgg	agtcattccta	660
aactccctta	aaacttacag	tcaagaagg	aggcataaag	tcctgtttac	ctgcagctcc	720
cacattatcg	tctttgccct	cttttttgtt	ccctgtat	tcattgtatgt	tagacctgtt	780
tcaaacatcc	ttttgataaa	ttcctgacag	tgttttatac	agttatcaca	cccatgttga	840
atcctttaat	atacacattg	agaaattcag	agatgagaaa	ttctgtagaa	acactcttgt	900
gtaaaagtta	actgtattag	agtaag				926

&lt;210&gt; 1049

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g899 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1049

atggaaagaa	tcaacagcac	actgttgact	gcgtttatcc	tgacaggaat	tccgtatcca	60
ctcaggctaa	ggacactctt	ttttgtgttc	ttttttctaa	tctacatcct	gactcagctg	120
ggaaacctgc	ttattttaat	caactgtctg	gcagacccaa	ggctccatgc	ccgccccatg	180
tacatctttc	ttgggtgttc	ctcagtcatt	gatatgagca	tctcctccat	cattgtccct	240
cgcctcatga	tgaacttcac	tttaggtgtc	aaacccatcc	catttggtgg	ctgtgttgct	300
caactctatt	tctatcactt	cctgggcagc	accagtgct	tcctctacac	cctaattggc	360
tatgacaggt	acctggcaat	atgtcagccc	ctgcgctacc	ctgtgctcat	gactgctaag	420
ctgagcgcct	tgtttgtggc	tggagcctgg	atggcaggat	ccatccatgg	ggctctccag	480
gccatccctaa	ccttcgcct	gccctactgt	gggcccattc	aggtggatta	cttcttctgt	540
gacatccctg	cagtgttgag	actggcctgt	gctgacacaa	cagtcaacga	gctggtgacg	600
tttgtagaca	ttgggtgtgt	ggttgccagt	tgcttctccc	tgatcctcct	ctcctacata	660
cagatcattc	aggccatcct	gagaatccac	acagctgatg	ggcggcgccg	ggctttttca	720
acttggtggag	cccattgtaac	cgtggtcacc	gtgtactatg	tgccctgtgc	cttcatctac	780
ctgaggcctg	aaaccaacag	ccccctggat	ggggcagctg	ccctagtccc	cacggccatc	840
actcctttcc	tcaacccctt	tatctacact	ctgcggaacc	aagaggtgaa	gctggccctg	900
aaaagaatgc	tcagaagccc	aagaactccg	agtgaagttt			939

&lt;210&gt; 1050

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g900 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1050

atgggaaaga	ccaaaaacac	atcgctggac	actgtggtga	gagatttcat	tcttctgggt	60
ttgtctcacc	ccccgaatat	aagaagcctc	ctcttctctg	tcttcttctg	cattttacatc	120
ctcactcagc	tggggaacct	gctcattctg	ctcaccgtgt	gggctgacct	gaagctccgt	180
gtcgcgccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctcctca	240
gtcatcgttc	cttgaattat	tttaaacttc	actcctgcca	acaaggctat	cccgttttgt	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacctcagt	cttctctctac	360
accttgatgg	cctatgacag	gtacctggca	atatgtcagc	ccctgcgcta	cccagtgctc	420
atgaatggga	ggttatgcac	agtccttctg	gctggagctt	gggtcgcccg	ctccatgcac	480
gggtctatcc	aggccacctt	gaccttccgc	ctgcctact	gtgggcccac	tcaggtagat	540
tactttatct	gtgacatccc	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagctttgtga	cctttgtgga	catcggggta	gtggccgcca	gttgcttcat	gttaattctg	660
ctctcgtatg	ccaacatagt	aaatgccatc	ctgaagatac	gcaccactga	tgggaggcgc	720
cgggccttct	ccacctgtgg	ctcccaccta	atcgtggcca	cagtctacta	tgtccctgt	780
atcttctatc	accttagggc	tggctccaaa	ggccccctgg	atggggcagc	ggctgtgttt	840
tacactgttg	tactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt	caagggactg	aatgaaaata	agta	954

&lt;210&gt; 1051

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g901 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1051

atgggaaaga	ccaaaaacac	atcgctggat	gccgtggtga	cagatttcat	tcttctgggt	60
ttgtctcacc	ccccaaatct	aagaagcctc	ctcttctctg	tcttcttcat	cattttacatc	120



ctcactcagc	tggggaacct	gctcattctg	ctcaccatgt	gggctgaccc	gaagctctgt	180
gctcgcacca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctcctca	240
gtcaccgttc	ctcggtttat	tttggatttt	actccttcca	tcaaggctat	cccgtttggt	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttccctctac	360
accttgatgg	cctatgacag	gtacctagca	atatgtcagc	ccctgcacta	cccagtgctc	420
atgaatggga	ggttatgcac	agtccttgtg	gctggagctt	gggtcgccgg	ctccatgcat	480
gggtctatcc	aggccacctt	gaccttccgc	ctgccctact	gtggggccaa	tcaggtggat	540
tactttatct	gtgacatccg	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagcttgtga	cctttgtgga	cgtcagggtg	gtggccgcca	gttgcttcat	gttaattctg	660
ctctcctatg	ccaacatagt	ccatgccatc	ctgaagatac	gcaccgctga	tgggaggcgc	720
cgggccttct	ccacctgtgg	ctcccaccta	atcgtggtca	cagtctacta	tgccccctgt	780
attttcatct	accttagggc	tggctccaaa	gaccccttgg	atggggcagc	ggctgtgttt	840
tacactgttg	tactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt				930

&lt;210&gt; 1052

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g902 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1052

atgtttatat	tgacaggctt	cacagatgat	tttgagctgc	aagtcttctt	atttttacta	60
ttttttgcaa	tctatctctt	taccttgata	ggcaatttag	ggctgggtgt	gttggtcatt	120
gaggattcct	ggctccacaa	ccccatgtat	tattttctta	gtgttttata	attcttggat	180
gcttgctatt	ctacagttgt	cactccaaaa	atgttgggtca	atttcctggc	aaaaaataaa	240
tccatttcat	ttatcggatg	tgcaacacag	atgcttcttt	ttgttacttt	tggaaactaca	300
gaatgttttc	tcttggctgc	aatggcttat	gatcactatg	tagccatcta	caaccctctc	360
ctgtattcag	tgagcatgtc	accagagtc	tatgtgccac	tcatactgc	ttcctacgtt	420
gctggcattt	tacatgctac	tatacatata	gtggctacat	ttagcctgtc	cttctgtgga	480
tccaatgaaa	ttaggcattg	cttttgtgat	atgcctctct	tccttgcctat	ttcttgttct	540
gacactcaca	caaaccagct	tctactcttc	tactttgtgg	gttctattga	gatagtcact	600
atcctgattg	tcctcatttc	ctgtgatttc	attctgttgt	ccattctgaa	gatgcattct	660
gctaagggaa	ggcaaaaagg	cttctctaca	tgtggctctc	acctaactgg	agtgacaatt	720
tatcatggaa	caattctcgt	cagttatatg	agaccaagtt	ccagctatgc	ttcagaccat	780
gacatcatag	tgtcaatatt	ttacacaatt	gtgattccca	agttgaatcc	catcatctat	840
agtttgagga	acaaagaagt	aaaaaaggca	gtgaagaaaa	tgttgaaatt	ggtttacaaa	900

&lt;210&gt; 1053

&lt;211&gt; 974

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g903 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1053

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccagt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acgggtgctga	ggaacttgct	gagcactctg	gctgtccgct	ctgagtcctc	gctccacaca	180
accatgtact	tcttctcttc	catcctgtgc	tgggctgaca	tcggtttcac	ctcagccaca	240
gttcccaaga	tgattgtgga	catgcagtg	tatagcaaag	tcattctctca	tgcgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	aggcatctgt	cgccctctgc	actaccagct	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
ctgcacagtt	ggattgtggt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctgttctg	acagcgtcat	caatagcate	600
ttcatatatt	ttggtagtac	tatgtttggt	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	tcgtcccttc	cattctaagg	atttcatcgt	cagatgggaa	gtataaagcc	720

ttctccacct	atggctctca	cctagcagtt	ttttgctgat	ttgatggaac	aggcattggc	780
gtgtacctga	cttcagctgt	ggcaccaccc	ctcaaggaat	gggtggtggtg	tgctcagtga	840
gtaagctgtg	gtcacccccc	atgccgaacc	ttttcatcta	cagcctggag	aaacagggac	900
atacaaagt	ccctgcgag	gctgcccac	aaaacagtcg	aatctcatga	tctgttccat	960
cctttttctg	gtgt					974

&lt;210&gt; 1054

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g904 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1054

gatacagacc	cacagagtat	aacagatgtc	tctatatctc	tcctcctcga	actctcagag	60
gatccagaac	tgcaaccggt	cgctcgctggg	ctgttcctgt	ccatgtgcct	cgctcatggg	120
ctggggaacc	tgctcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgctt	gacatcggtt	tcacctccac	caeggtcccc	240
aagatgattg	tggaacatca	gtctcacagc	aaagtcattt	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tgaggcatg	gaaaaaagac	atgtcctcga	gtgtgatggc	360
ctatgaccgg	tttgtaccca	tctgtcacc	tctatatcgc	tcagccatct	tgaaccctgt	420
tttctgtggc	ttcctaaatt	tggtgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	tttccctgct	gccgtatttg	gttttcttcc	catctcgggg	acccttttct	660
cttactgtaa	aatggtttcc	tccattctga	gggtttcatt	atcagggtgg	aagtataaac	720
cttctccacc	tgaggggtccc	acctgtcagt	tggttgctga	ttttatggaa	caggcggttg	780
agagtacctc	gggttcagatg	tgctcatctt	cccagagaaag	gggtgcagtg	cctcagtgat	840
gtacacgggtg	gtcaccacca	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcgggcgg	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaa		1006

&lt;210&gt; 1055

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g905 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1055

atggaaaata	ggaaaaattg	acttaattca	tcctcttggg	gtcacacag	aaccctgagg	60
gccaaaaagt	tttatttgtc	acattcttac	tcattctacat	tgtgacgata	atgggcaacc	120
tccttatcat	ggtgaccatc	atggccagcc	agtccttggg	ttcccccatg	tacttttttc	180
tggttctctt	atcattttata	cataccgtct	attatactgc	cattgtctccc	aaaatgattg	240
ttgacctgct	ctctgagaaa	aagaccattt	cttttcaggg	ttgtatggct	caacttttta	300
tggtatcatt	atttgctggg	gctgaagtca	ttcttctggg	ggtaatggcc	tatgatcaat	360
atgtggccat	ctgtaagcct	cttcattatt	tgatcatcat	gaatcgtcga	gtctgtgttc	420
tcattgctgt	gggtggcctg	attggaggct	ttcttctact	attggttcaa	tttctcttta	480
tttatcagct	ccctttctgt	ggacccaatg	tcattgacaa	cttctctgtg	gatttgtatc	540
ccttattgaa	acttgcttgc	accaatacct	atgtcactgg	gctttctatg	atagctaatt	600
gtggagcgat	ttgtactgtc	accttcttcc	ctctcctgct	ttcctatggg	gtcatattac	660
cctctcttaa	gactcagagt	ttggaaggga	aatgcaaagc	tttctacacc	tgtgcatccc	720
acatcactgt	gatcacttta	ttctttgtcc	cctgcatctt	cctgttagca	aggcccaact	780
ccacctttcc	cattgataaa	tccatgactg	tggttttaac	ttgtataact	cccatgctga	840
aaccactaat	ctatgccctg	aggaatgcag	aatgaaaag	tgccatgagg	aaactttgga	900
gtgaaaaagt	aagcttagct	ggaaaaagg				929

&lt;210&gt; 1056

&lt;211&gt; 925

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g906 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1056

cacatgcctc	ccaacaatgt	gactgaattc	attctcttgg	ggctcacaca	gaatccacac	60
ttgcagaaaa	tactctttat	tgtattttta	tttatttttc	tatttaccat	gctggccaat	120
ctgttcattg	tcatcaccat	ctcctgtagc	cccacacttt	catcacccat	gtacttcttt	180
ctcacttact	tatcctttat	agatgcctcc	tacacctctg	tcacaacccc	caaaatgac	240
accgacctgc	tctaccagag	gagaactatt	tccttggctg	gctgcctgac	tcagctcttt	300
gtggagcact	tgctgggagg	ctcagagatc	atcctcctta	ttgtcatggc	ctatgaccgc	360
tacgtggcca	tctgcaagcc	cctgcactac	acaaccatta	tgcaacaagg	gatctgccac	420
cttctgggtg	tgatagcctg	gattggaggc	atcctgcatg	ccactgtgca	gattcttttc	480
atgaccgact	tgcccttctg	tggtccccaa	tgctattgac	cactttatgt	gtgatctctt	540
cccattgttg	aaacttgcc	gcagagacac	ctacagactt	gggatgctgg	tggcagccaa	600
cagtggagcc	atgtgcttgc	tcatcttttc	cctgctcgtc	atctcctaca	tagtcacctc	660
gagctccctg	aaatcctata	gctctgaagg	acagcacaaa	gccctctcca	cctgtggctc	720
ccactttact	gtcgtgtgac	tcttttttgt	gccttgcata	ttcacctaca	tgcatacctgt	780
ggtcacctac	tctgtggaca	agttgggtgac	tgtgttcttt	gcaatcctca	ctcccatggt	840
aaatcctata	atttacactg	tgagaaacac	agaggtaaaa	aatgccgtga	ggagtttgtt	900
gaggaaaaga	gtaacagttt	atgca				925

&lt;210&gt; 1057

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g907 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1057

atgtacacga	ctttactcat	ggcccagggt	gtgtctctgt	gcagacaatg	gatccacac	60
tctttctgtg	atatgtctgc	tctgtctgaag	ctggccctct	ctgacactcg	agttaatgaa	120
tgagtgatat	ttatcatggg	agggtcatt	cttgtcatcc	catccatact	catccttggg	180
tcctatgcaa	gaattgtctc	ctccatcctc	aagggtccct	cttctaagtg	tatctgcaag	240
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tggtctctac	ttatgctcat	cagctaatag	ttctactcta	aaggacactg	tcatggctat	360
gatgtacact	gtggtgaccc	ccatgctgaa	ccccctcatc	tacagcctga	ggaacagaga	420
catgaaggga	gccctgagca	gagtcattca	tcagaagaaa	actttcttct	ctctctgatg	480
ataacacttg	gagctatta					499

&lt;210&gt; 1058

&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g908 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1058

atgggaccaa	agaatctaac	tcgtgttttg	gaattcttcc	tcctccactt	cttagatgac	60
ttggaactgc	agcctttcct	cttcaggctg	tcctgaacc	atgcacctag	tcacagtgtc	120
tgcgaacttg	ctcacatcct	tctgactgtc	agctttgccc	tcacctccac	aaccccatga	180
acttcaacct	gtccttagct	gacattgggt	tcacctctgc	cacaatttca	aagataactg	240
tagacctcca	aactcacagc	agaatcattt	tatacatgag	ctgcctgaaa	tagatgtctt	300
ttaaaattat	ttttggatgt	ttgcacaatc	tactcatgac	tgtgatggcc	tatgacccat	360
ttgtggcgac	ctgtcatctc	ttgtactaca	cagtgatcag	gaatccccac	ctctgtggcc	420
tctgtcttct	ggctctcttc	tctctctctc	tttttttttt	ttgatcagtc	ttttggaaac	480
ccagctgtac	agtttgatgg	tgtcacaagt	tctctcatgc	aaatgtagac	attcctcatt	540

tcttctgtga	cccttctcag	tttctccacc	tttctgttgc	tgacactgcc	accaataaca	600
cattaatgca	ttttattggt	gccatctctg	tgggtccattc	tcagggatcc	tttactgtta	660
tactcaaatt	atgttctcca	tactcataac	cctataaaat	gtgggaagta	taaagcaaac	720
cttctccacc	catcgctctc	acctgtcagt	tgtttgttta	ttttatggaa	caggccttgg	780
agtatacctt	agtttggtcg	gctcaccttc	cccaagaaca	ggtgtggtgg	cctcaatggt	840
atataccaca	gtcaccctca	tggtgaaccc	tgcatccaca	gcctgaggaa	cagagacatc	900
aagaatacct	ggtggtggct	cctcagcata	actgcctggt	atcaatacct	gtgctatcct	960
ttatggagtg	tggttagaaa	aaacagcaaa	ctcaaa			996

&lt;210&gt; 1059

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g909 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1059

atggggactt	caaataatga	gactgaattc	attcttttgg	gcattacaaa	aaatccagaa	60
ctaaggaaaa	tattctctgc	tttgtttcta	gccatgtatg	tgaccacagt	gttgggaaat	120
ctattcattg	tgggtgactct	ggctgcaagt	tggagtctga	gatcacctat	gtacttttcc	180
cttacttctt	tgtctctcat	gggtgccacc	tactcttcca	tcactgcccc	taagatgact	240
gtggactctt	tgagaacact	accatttccc	ttgaaggctg	catgaccag	ctctttgcag	300
agcatttctc	tgatgggtga	gcgatcatcc	ttctcactgt	gatggctctg	gactgctatg	360
aggccatcag	taagcccctg	catgacacaa	ccatcatgag	tccacgggtg	tgctgctgtt	420
ggtggtagaa	gcttgggtgg	ggggattaac	acatgccaca	atacagcttt	ttttttttca	480
tatatcaaat	acccttctgt	ggtcccaata	ttattgacca	ttttatatgt	gatttgtttc	540
cattgttaaa	acttgcttac	atggacaccc	acatgctggg	tctcttagtc	atcctcaaca	600
gtgggggtgat	gtgtatggcc	atcttccctta	tcctaattgc	atcctacatt	gtcaccctgt	660
actctctgaa	gtcttgcagc	tcggtaggtc	gacgcaaac	actttccacc	tgtggctccc	720
accacacagt	ggtcatcttg	ttcttcgtgg	agtgtatttt	cttgtagata	agacctgttg	780
tcacttaccc	catagacaag	gatatggcta	tttcttttac	tattgttgca	cccatgttaa	840
atcctctgat	ctataccctg	aggggcatca	aggtaaaaaa	tgccataaga	aaaatgtgga	900
tgaaacaggg	gaccctaggt	ggt				923

&lt;210&gt; 1060

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g910 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1060

atggctccga	ccaacctcac	atctgcccc	gctgttcttc	ctcctcggcc	tggtggacgg	60
aacagacgcc	caccgctgc	tgttctctgt	ctgccttggg	tctatctgct	caacgccctg	120
agcaacctga	gcatggtggc	gctggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcactgagc	ctcgtggacg	tctgctttac	caccgtcacg	gtccccaggg	240
tgctggccgg	cctgtctccac	ccgggccagg	ccatatacct	ccaggcgtgt	ctgccgagat	300
gtacttcttc	gtgactctgg	catcacccag	agctacctca	tggcggccat	gtcctagcga	360
gcccgaaggg	gcgtgccggc	acctctgtac	ggcgcgctgg	tgacgccatc	ggcgtgcgcc	420
tgctggtgcg	tcgctcgtgg	gccgtgacgc	acctgcactc	gctgctgcac	acgctgctcc	480
tctccgcgct	ctcctacccc	tacccacccc	ccgtgcgccc	cttcttttgc	gacatgacgg	540
tgatgctgag	cttggcgacc	tcggacacgt	ccgcgcggga	gacggccatc	ttctccgagg	600
gcctggccgt	ggtgttgccc	ccgctgctcc	tcgtgttcc	tttctacgc	gcgcacctctg	660
gtcgcggtgc	tcggttgccg	cgccgcgcgc	gcgccttctc	cacctgcggg	gcccacctag	720
tggcgggtgg	ggtggcgctt	ttctttggct	ctgtcctctc	cgtgtatttc	ccgccgtcgt	780
ctgcctaact	agcccgctac	gaccgcctgg	ccagcgtggt	ctacgctgtc	atcacgccga	840
ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	caagggcgcc	ctgaaaaggg	900
ggctcagcat	ggagggctgc	accccaagag	gcgtgagggc	aaatctggct		950

<210> 1061  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g911 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1061  
 atgaaagggg caaacctgag ccaaggggatg gagtttgagc tcttgggcct caccactgac 60  
 ccccagctcc agaggctgct cttcgtgggtg ttccctgggca tgtacacagc cactctgctg 120  
 gggaacctgg tcatgttccct cctgatccat gtgagtgcca ccctgcacac acccatgtac 180  
 tccctcctga agagcctctc cttcttggat ttctgctact cctccacggg tgtgccccag 240  
 accctgggtga acttcttggc caagaggaaa gtgatctctt attttggctg catgactcag 300  
 atgttcttct atgcgggttt tgccaccagt gagtgctatc tcatcgctgc catggcctat 360  
 gaccgctatg ccgctatttg taaccccctg ctctactcaa ccatcatgtc tcctgaggtc 420  
 tgtgcctcgc tgattgtggg ctccctacagt gcaggattcc tcaattctct tatccacact 480  
 ggctgtatct ttagtctgaa attctgcggt gctcatgtcg tcaactcact cttctgtgat 540  
 gggccaccca tccgttcctt gtcttgtgta gacacctcac tgtgtgagat cctgctcttc 600  
 atttttgctg gtttcaacct tttgagctgc accctcacca tcttgatctc ctacttctta 660  
 attctcaaca ccactctgaa aatgagctcg gcccagggca gggttaaggc attttccacc 720  
 tgtgcatccc acctcactgc catctgcctc ttctttggca caacactttt tatgtacctg 780  
 cgccccaggt ccagctactc cttgaccacg gaccgcacag ttgctgtcat ctacacagtg 840  
 gtgatcccag tgctgaaccc cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900  
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062  
 <211> 948  
 <212> DNA  
 <213> Unknown (H38g912 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1062  
 atgcaaaaacc aaagctttgt aactgagttt gtcctcctgg gactttcaca gaatccaaat 60  
 gttcaggaaa tagtatttgt tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120  
 atgctaattg tagtaacctt tctcagcagc cctgctcttc tgggtgtctc tatgtacttc 180  
 ttcttggggt tccgtgcctt cctggatgag tgcttctcat ctgtcatcac cccaaagatg 240  
 attgtagact cctctatgtg gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300  
 tttgctgaac acttctttgc tgggggtggag gtgattgtcc tcacagccat ggcctatgat 360  
 cgttatgtgg ccatttgcaa gcccttgcat tactcttcta tcatgaacag gaggctctgt 420  
 ggcattctga tgggggttagc ctggacaggg ggcccttgct attccatgat acaaattctt 480  
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcactttat gtgtgacttg 540  
 taccggttac tggagcttgc ctgcactgat actcacatct ttggcctcat ggtggtcatc 600  
 aacagtgggt ttatctgcat cataaacttc tccctgttgc ttgtctccta tgctgtcatc 660  
 ttgtctcttc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720  
 tctcacattg ctgttgtgat tttgttcttt gtcccatgca tatttgtata tacacgacct 780  
 ccactgtctt ttcccttga caaaatggcg gcaatatttt atatcatctt aaatcccttg 840  
 ctcaatcctt tgatttacac tttcaggaat aaggaagtaa aacaggccat gaggagaata 900  
 tggaacagac tgatggtggt ttctgatgag aaagaaaata ttaaactt 948

<210> 1063  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g913 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1063

atgcaactga	ataataatgt	gactgagttc	attctgcttg	gattgacaca	ggatccctttt	60
tggaagaaaa	tagtggttgt	tatttttttg	cgtctctact	tggaacact	gttgggtaat	120
ttgctaataca	ttattagtgt	caaggccagc	caggcactta	agaacccaat	gttcttcttc	180
cttttctact	tatccttate	tgatacttgc	ctctctactt	ccatagcccc	tagaatgatt	240
gtggatgcc	ttttgaagaa	gacaactate	tccttcagcg	agtgcagat	ccaagtcttt	300
tcatcccatg	tctttggctg	cctggagatc	ttcatcctca	tcctcacggc	tgttgaccgc	360
tatgtggaca	tctgtaagcc	cctgcactac	atgaccatca	taagccagt	ggtctgtggt	420
gttttgatgg	ctgtggcctg	ggtgggatcc	tgtgtgcatt	ctttagttca	gatttttctt	480
gccttgaggt	tgccattctg	tggccccaat	gtgatcaatc	actgtttctg	tgacttgcag	540
cccttggtga	aacaagcctg	ttcagaaacc	tatgtgggta	acctactcct	ggtttccaat	600
agtggggcca	tttgtgcagt	gagttatgtc	atgctaatat	tctcctatgt	catcttcttg	660
cattctctga	gaaaccacag	tgtgaagtg	ataaagaaag	cactttccac	atgtgtctcc	720
cacatcattg	tggtcatctt	gttctttgga	ccttgcata	ttatgtacac	atgccctgca	780
accgtattcc	ccatggataa	gatgatagct	gtattttata	cagttggaac	atcttttctc	840
aaccctgtga	tttacacgct	gaagaatata	gaagtgaaaa	gtgccatgag	gaagctttgg	900
agcaagaaat	tgatcacaga	tgacaaaaga				930

&lt;210&gt; 1064

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g914 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1064

atggagacaa	caaatacctc	tgccgtgact	gaattctttc	tggtggggct	ttcccaatat	60
ccagagctcc	agctttttct	gttcctgtct	tgccctcatca	tgtacatgat	aatcctcctg	120
ggaaatatgt	tcctcattat	catcaccatc	ttggattctc	gcctccatac	ccccatgtat	180
ttctttcttg	gaaacctctc	attcttgggc	atctgttaca	catcatcatc	cattcctcca	240
atgctttatta	tatttgtatc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atggttgtgt	cccttggctt	gggctccatt	gagtgatctc	tcctggctgt	gatggcctat	360
gaccgctatg	tggccatctg	caacccactg	aggtactcca	tcacatgaa	cagagtgtctg	420
tatgtgcaaa	tggctgcatg	gtcctggatc	ataggctgtc	tgacctccct	attgcgaaca	480
gttctgacaa	tgatgttgcc	tttctgtggg	aataatatca	ttgatcatct	tacctgtgag	540
atcctggctc	ttcttaaagt	catatgtctc	gatatctcca	taaatgtgtt	tataatgaca	600
gtgtcaagta	ttgttttatt	ggtgattcct	cttaattttt	atctcctatg	tgtttattct	660
ctcttccatc	ttgagaatta	attctgctga	gggaagaaag	aaagcctttt	ttacctgttc	720
agcgcacttg	actgtgggta	tcttattcta	tggttcagtt	cttttcatgc	acatgaagcc	780
caaatacaag	ttcacacag	catctgatga	aatcattgga	ttgtcttatg	aagtgatcac	840
cccaatgaac	cccatcatct	acagcctgag	gaataaggag	ataaaaagaag	ctgtgaagaa	900
aatcctcagc	agacacgtgc	atctatggaa	aatatgaaag	gccttgaggc	atgtgacgtt	960
ctca						964

&lt;210&gt; 1065

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g915 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(620)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1065

gatgcagct	cgagcgcccc	cagtgatgat	gatatctgca	gaattcgccc	ttccaatgta	60
ctttttcctg	aagaacctct	ctgttttgga	tctgtgctac	atctcagtea	ctgtgcctaa	120
atccatccgt	aactccctga	ctcgcagaag	ctccatctct	tatcttggct	gtgtggctca	180
agcctatttt	ttctctgcct	ttgcatctgc	tgagctggcc	ttccttactg	tcattgtctta	240

tgaccgctat	gttgccattt	gccaccccct	ccaatacaga	gccgtgatga	catcaggagg	300
gtgctatcag	atggcagtc	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggcaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tcttccgtga	420
catccctcag	gtgttgcccc	tggtttctctg	ngagggttttc	tttgtagagc	tttgacccng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anatcttctn	aangggggctc	nagaatccct	tnaggaccag	antcnagcta	aaagcctttn	600
cccnctgct	tcceccacg					620

&lt;210&gt; 1066

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g916 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(611)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1066

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	cttccaatgt	60
atattttct	ctctgacctc	tccttcttgg	acctctgctt	taccacaagt	tgtgtccccc	120
agatgctggg	caacctctgg	ggcccaaaga	agaccatcag	cttcctggga	tgctctgtcc	180
agctcttcat	cttcctgtcc	ctggggacca	ctgagtgcac	cctcctgaca	gtgatggcct	240
ttgaccgata	cgtggctgtc	tgccagcccc	tccactatgc	caccatcatc	cacccccgcc	300
tgtgctggca	gctggcatct	gtggcctggg	ttatgagtct	ggttcaatcg	atagtccaga	360
catcatccac	cctccacttg	cccttctgtc	cccaccagca	gatagatgac	tttttatgtg	420
aggteccatc	tctgattcga	ctctcctgng	gagatacctc	ctacaatgaa	atccagttgn	480
ctgtgtccag	tgtcatcttt	ggtggntgtg	cctctcagcc	tcateccttg	ctcttatgga	540
gccactgccc	aggcnggggc	tgaggattaa	ctttgccnna	gccatggaag	aaaggtcttt	600
nggacctngn	n					611

&lt;210&gt; 1067

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g917 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(619)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1067

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	ctttctttat	60
ttcgaagagt	atacactagt	ggattgaaga	gaaacaaata	cataggaagg	gcgaattcca	120
gcacactggc	ggccgttact	agtggatccg	agctcggtac	caagcttgat	gcatagcttg	180
agtattctaa	cgcgtcacct	aaatagcttg	gcgtaatcat	ggcatagct	gtttcctgtg	240
tgaaattggt	atccgctcac	aattccacac	aacatacgag	ccggaagcat	aaagtgtaaa	300
gcctgggggtg	cctaagtgtg	gagctaactc	acattaattg	cgttgcgctc	actgtccgct	360
ttccagtcgg	gaaacctgtc	gtgccagctg	cattaatgaa	tcggccaacg	cgcnngnaga	420
ggccggnntg	cgtattgggc	gctcttccgc	ttctcgctca	ctgactcgct	gcgctcggga	480
cgctcgggctg	cggcgagcgg	tatcagctta	ctcaanggcc	gtantacggt	tattencagg	540
aatnnggggt	taacgcngg	naaagaacat	tgtgngccan	angncaagcn	taatgcccag	600
gaaccgntan	aacgntccc					619

&lt;210&gt; 1068

&lt;211&gt; 621

&lt;212&gt; DNA

<213> Unknown (H38g918 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

gnnnnntntt cantccattg ggcctcttag atgcatgctc gagcggccgc cagtgtgatg	60
gatatctgca gaattcgccc ttattccgga gggatacat gaagggattg gtaactagac	120
gtaaactcga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa	180
gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag	240
actctgaaag aggtggaagg gattgaatac aatcaaaagt atggtgactg ctagttccaa	300
gatggtggcg taggggcaag ctggctttgc ttacccccct ggcagaaaac caaaaacaaa	360
tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc	420
cagggcccgag agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt	480
tctaaggagg acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc	540
cataaaacaa agattggaaa atgttgaatt ttgcaaccag gagcaaatac tgggaaaggc	600
gaattccagc cacttgcnge c	621

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

gnnnnntnan tcantgcct ngggccctct agatgcatgc tcgagcggcc gccagtgtga	60
tggatatctg cagaattcgc ccttggtgcg caaggtgtaa atgaaagggg ttgcgaggga	120
gtaaatgaag ggattacgca ggagtaaatt aagggtattac gcaggagtaa atgaagggat	180
tacgcaggag taaatgaagg gattacgcag gagtaaattga agggattacg caggagtaaa	240
tgaagggatt acgcaggagt aaatgaaggg attacgcagg agtaaatgaa gggattacgc	300
aggagtaaat gaagggatta cgcaggagta aatgaaggga ttacgcagga gtaaatgaag	360
ggattacgca ggagcaata cataggaagg gcgaattcca gcacactggc ggccgttact	420
agtggtaccg agctcggtac caagcttgat gcatagcttg agtattctaa cgcgtcacct	480
aaatagcttg gcgtaaatcat ggtcatagct gtttctctgt tgaaattgtt atccgctcac	540
aattccacac aacatacgag cccggaagca taaagtgtaa agnctggggg gcctaattgag	600
tgacttactc catta	615

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

ggnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatatc	60
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tgcagaattc	gcccttccga	tgtattttct	tctacgttaa	ggatttttaa	attgttacta	120
atgcataagg	gcaacacatt	ctgtaatgct	gacaagatga	aagagccaaa	agtaattaat	180
gatgctgtta	cctcacaaat	atgtatgtgt	ggatgtatat	atatctattc	aatatatgta	240
actatacata	tgtctgtttc	taattgaaaa	caccaggtaa	ttatcatctg	tagaaaccct	300
agtgtctcag	ataagttggc	tagttttttg	tttcacataa	aggaacaaac	atttatagat	360
ttatatgtat	attaaaaatg	gtaaaaattg	gctgggtgca	gtgggttcag	cctataatac	420
cagcactttg	ggaagccgag	gtgggcgcat	tacttgaggt	aaggagccca	gcctgaccaa	480
caaggtgaaa	ccccatccct	actaaaaata	caagaattag	cccggggatg	gtgggtggcca	540
cctgtaatcc	cagctacttg	ggagactgaa	gccaggaaaa	tcacttgacc	caggaagcng	600
aggttgcagg	ngag					614

&lt;210&gt; 1071

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g921 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(857)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1071

atggnnnnnn	nntttnnnaa	anttttnccc	antttgggcc	gnccccccct	tctttaagg	60
aatgggcccc	ttgggccctt	cccggaaggc	ccggggggcnc	ccggccccca	aggtttgggt	120
tgggaaatgg	ggggaattta	aattcctttg	ggccaaggna	aaaattttcc	ngccccccct	180
tttttccccct	tttggttttt	anccggggga	anggggggggt	tgattaatta	atcgggaagn	240
tnnggggggaa	ntttttttaa	aaaaaccttg	ggggaagggt	ccaacccaac	aaggttgggt	300
ttccanggga	cgttggggac	caggcttttn	gaatcaagaa	tcccaaagg	cattcttttg	360
gattaaggaa	nggtgccggg	accggtgaaa	gggaaaaaac	tgggtggacc	cataccaaaa	420
tgagaaccac	ggtgagatgc	cgaggagcac	gtggagaaag	gctttgcttc	cggccactgg	480
cagaggggat	cctgaggatg	gtgcttgatg	atgtacacat	agggagacaa	gggtgatgag	540
gcatgaactc	aggataacca	caacagcnat	cacaaaggcc	acaaagctct	actgcctgtg	600
tgttgggtgc	aggccagggc	aatccagggg	tgcaatgtca	caagaaagaa	agtgggtgat	660
ggcacgggng	ggccacagaa	ggacaggcca	cttgatgaag	ggcttgtggg	cactgcaatg	720
gccacgaaac	caccagacc	aggaaccan	ggccaagctt	gcgcctgaag	agcaaggcta	780
ctcatgaatg	gcttccttag	tngtaaagga	tagcaagatg	gcaaaggcaa	gccggtcatn	840
aagccatggc	ttgcng					857

&lt;210&gt; 1072

&lt;211&gt; 593

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g922 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(593)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1072

aacgcagagt	accgcccact	acgtaatctg	tacatgaaag	ggtttaaaaag	agactgggaa	60
gagaggaatt	ggcaagatca	agcagaggca	actccttcta	gtccttctag	taccgcaagg	120
ggcagataaa	tggaatgggt	aacacctaga	ggaaagtata	cttgccaaaa	gcaaatncat	180
aggggggagt	acattatcgg	gttgaaaaaa	gtattccatg	cagataaaaa	ccaaaagcaa	240
atacatcggg	ggcgctacttc	tgctgtcttt	gagcgctactg	atggtaccca	gcttttgntc	300
ctttagttag	ggtaattg	gcgcttgccg	taatcatggt	catagctggt	ttctgtgtga	360
aattgttatc	ccgctcacaa	ttcacacaac	atacagccc	gggagcataa	agtgtaaagc	420
ctgggggtgcc	taatgagtgg	agcttactta	cattaaattg	cgttgcgctc	actggccgct	480

tttccaagtc	gggaaacctg	tcgtgncagc	ttcantaatg	aatcggccaa	cgccgcgggg	540
agaggcgggt	tgcgtattgg	gcgctcttcc	gcttcttngt	tnactgactt	cgg	593

&lt;210&gt; 1073

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g923 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(624)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1073

gnnntttaac	nccggngetn	cnagcagtg	aacaacgcag	agtacgcccc	cgatgtactt	60
tctttttcag	tctcaagtct	tcctcttctc	caaagatttt	gtcttttcta	ctacctgagc	120
taccaaatcc	cttgatcatca	atttcaataa	ctgtattctc	ttcatcattt	caacttcaaa	180
cgtgtcatct	cagaacaagc	ttcatgttac	ttccaatttt	atccttcttg	tttgctgatt	240
ccaagaattc	cagtcccatc	taggcccgcga	atgcattgtt	cctgccaccc	ttttcatatc	300
ctcaattccc	ttgtatcatc	actttccttt	tatatagcac	agattccatg	attcataaca	360
ataaattatgt	ttttttttgc	atgtgctctt	aatttccttt	cttgctccta	ttatcttcta	420
tcatactttt	ctggaaacac	taattctggg	gaaatatact	ctttgtggac	tttgacttta	480
tgctcagtc	gctgaagatg	atggctagac	aaatactcac	aatcatgctg	actggcccaa	540
tttatagtca	tgaccaccga	ttacaaaccc	cttcatttat	tctccgcaac	aggggcgtct	600
tctgcgcttg	agcgtccggg	gggg				624

&lt;210&gt; 1074

&lt;211&gt; 637

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g924 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(637)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1074

ttatnnccat	tggagctcca	aagcagtggt	aacaaccgca	gagtacgccc	cccatgtatt	60
ttctttttct	tggggnagct	gnatgcttcc	tnctggctac	catggnatat	gaccggctat	120
gnngncatct	gcagtcctt	gnnctcccag	tcattatgaa	ccaaaggaca	cgggccaaac	180
tggtggtgn	ttcctgggtc	ccaagctttc	ctgnagctac	tgngcaagac	cacaatggct	240
cttnagnttt	ccattctgng	gcaccaacaa	ggtgaaccac	ttntttctgn	gacagccggc	300
tgtgctgaaa	gctggtctgn	tgcaagacac	agcactgttt	gagatctacg	ccatcgctcg	360
aaccattctg	gtggtcaatg	aacccctgct	tgctgatctt	gngttcctat	actcgnattg	420
gtgctgctat	ccctcaagaa	cccatcaagc	taaangggaa	gcaataaagn	cctttctcta	480
cgtgctcctt	aacacctccc	ttggtggcct	ctcttttcta	atataatcnt	ctaagcctca	540
acctaattct	tgggectnaa	ntcaaataaa	ttcttctgga	gaggcaagaa	ggtgggtattc	600
atttatncta	cactggtngn	gactccatgn	tgggaact			637

&lt;210&gt; 1075

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g925 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

<221> misc\_feature  
 <222> (1)...(621)  
 <223> n = A,T,C or G

<400> 1075  
 gtnatnccnt ttaatnccnt tggagctcca agcagtggtta acaacgcaga gtacgcccgt 60  
 tcctcagaca gtatatgaat gggttaaaaa tgggccagag cagatgcagg aagatcaaatt 120  
 aggaggctac tgcagtagag tcaaattctag ggctgatggt ttcttgggat gcatagtaatt 180  
 aggtagatag agaaagtctt taggaggttag aatggacagg acttcacaaat gcattaaattg 240  
 tagggagaaa aaaaatgatt cctgggtttc tagcttgagc tagtagggat agtggtagaa 300  
 ttactgata tggaaaactg gaggaaaaaag agtttggag agaaagatgg caagttaaatt 360  
 acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag 420  
 ccatgggcta ggaacataca gtgggattcc ctggcatgtc attgggttact gaagtcagag 480  
 tgtatgagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg 540  
 gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttngaa 600  
 aaggagagaaa nggttgaaatt t 621

<210> 1076  
 <211> 631  
 <212> DNA  
 <213> Unknown (H38g926 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(631)  
 <223> n = A,T,C or G

<400> 1076  
 ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag 60  
 cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt 120  
 gtccctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aagggtgcat 180  
 agtagaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttcttcctt 240  
 ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaaa 300  
 tgaagggaaa cacaagaaaa atggtggtgc tcaaaaacac cgtgcactca tagaccagg 360  
 tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc 420  
 tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc 480  
 ctatcatcca agatcctgtt atcatcagtg cacacactct tttctcata cggatgagat 540  
 agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg 600  
 cttctgcacc tgctaaagtc aggaagaaga t 631

<210> 1077  
 <211> 620  
 <212> DNA  
 <213> Unknown (H38g927 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(620)  
 <223> n = A,T,C or G

<400> 1077  
 tgttantccn ntttntncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc 60  
 ctccctgttt ctgagagtgt agatgaaggg gttataggag ataaagatca gggcaatatg 120  
 taggacaagg acacagacac tgacaacaaa gttgattatc tcattgacag tgggtgtctgt 180  
 gcaggccagc ttcagcaggg gtctcacatc acagaagaag tgggagatga caaagtcac 240  
 acaaaagggc aggccaaaca tagatgttac ttggacaata gccatgcccc ggccaatcct 300  
 cagtgaacca gatccagtc agacacaagc cctcttacct atgaataccg taagggggtg 360

cagaagacca	catagcaatc	atatacccatg	gctatgagaa	gaaagcagtt	gttgatgcc	420
aaagtccat	agaagagctg	agtgcacacg	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcaggtctc	agagatagac	540
agcaatgctt	aggaaaaagt	acatgggccg	tacttctgtc	gtcttgagcg	tactgatggt	600
accagctttt	tgttcccttt					620

&lt;210&gt; 1078

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g928 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(627)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1078

tgtagctcca	aagcagtggg	aacaacgcag	agtacgcctt	cttggttacg	taaggggaata	60
gatgatggg	ttcagcatgg	gggtgactac	agtgtacatg	acagtggcca	cacgggtccca	120
ctctgtctgc	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gttcaccaca	nccagggtgg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggc	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggncct	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgcngcgcc	ctnggtgaag	atgagcagct	tggatgtggt	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtgggngc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgctcgtggg	acaccagcca	tgccattcca	accagggctg	cgcacatngc	cggggacatt	540
ctcgtgggat	aaggggaagg	gtgccggatn	ggcacgtatc	agtcataggc	cttggncgcc	600
agaagacagc	tttnaattta	ccccagg				627

&lt;210&gt; 1079

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g929 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1079

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgaactg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggcccagctc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttctctcg	180
gagcattgag	tgcttcttgt	ttacggtgat	ggcctatgac	cgcttcaactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaaccc	aaggatctgt	gtggccctgg	ctgtgggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtgggtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttggcc	tcatactctt	480
ggctgctttc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

&lt;210&gt; 1080

&lt;211&gt; 616

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g930 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(616)

<223> n = A,T,C or G

<400> 1080

gnnnnnnnnnt	tcatnccatt	gggccctcta	gatgcatgct	cgagcggccg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttgttgctt	agagtgtaaa	taaaagggtt	aacattggct	120
tagagggtgaa	gagtaaatac	ataggaaggg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcgggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttcctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgtt	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaaacgc	gcggggagag	gcggtttgcg	tattgggcgc	480
tcttcgctt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggtcgcg	gcgagcggta	540
tcaagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

ngnnnnnttna	ntcnangeen	ngngccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttccaatg	tatttacttc	tcagccagct	ctcccttatg	120
gacctgatgt	acatctccac	caccgtcccc	aagatggcgt	acaacttcct	gtccggccag	180
aaaggcatct	ccttcctggg	atgtggtgtg	caaagcttct	tcttcctgac	catggcgtgt	240
tctgaaggct	tactcctgac	ctccatggcc	tacgaccgtt	atttggccat	ctgccactct	300
ctctattatc	ctatccgcat	gagtaaaatg	atgtgtgtga	agatgattgg	aggctcttgg	360
acactggggg	ccatcaactc	cttggcacac	acagtctttg	cccttcatat	tccctactgc	420
aggtctaggg	ctattgacca	tttcttctgc	gatgtcccag	ccatgttgct	tcttgctgtg	480
cagatacttg	ggtctatgaa	tatatggttt	ttgtaaggac	aaagcctctt	tcttcttttn	540
cctttcattg	gcatacttc	ttctgngggc	cgagtccata	ttgctggcta	tataatgcac	600
tcaaaggagg	ggagg					615

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

gnnnnnnnat	ttnatgcct	tnttgattcc	cnttnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttcccac	acttctctat	taagaagcat	gtgagatact	180
tgttacaaac	ataacatcct	ggtccacccc	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tgttggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactggtag	cagggttgag	360
gatcacagg	aagagggtaa	gcataatcaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccatgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480

ctctgaggaa	caagggggcg	tactttctgtc	gtcttgagcg	tactgatggg	acccagcttt	540
tgccccctta	gtgagggtta	attgcgcgct	tggcgtaatc	atgggtcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

<210> 1083  
 <211> 613  
 <212> DNA  
 <213> Unknown (H38g933 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(613)  
 <223> n = A,T,C or G

<400> 1083	
annncntng	gagctccaaa
gcagtggtaa	caacgcagag
tacgccccct	atgtacttac
60	
ttttgttaag	tccaacctcc
atcctccttg	gccttttgat
tcaattgatc	actccttcct
120	
cctcaaaaca	ccttggtcac
tcatectttc	tcagtcctct
ttgtggattc	ttcctcattt
180	
atgtgacctc	ttgtggtga
accctttcat	atacactctc
cgtaacaaag	agggcggtact
240	
tctgtcgtct	tgagcgnact
gatggnaccc	agcttttggt
cccttttagtg	agggntaatt
300	
gcgcgcttgg	cgnaatcatg
gncatagctg	nttnctgngn
gaaantgnta	tttcgntnac
360	
aattncacac	aacatacnag
ccgggagcat	aaaggggnnaa
gncctggggg	gcctaataag
420	
ggagcttact	cacaataatt
ggggtgngcc	cactggcccc
ttttcaggcg	ggaaaacctn
480	
gcggggccag	ctggaataaa
tgaatcgggc	cacgcgccgg
ggaggagggc	gggttnngga
540	
attgggcgct	ttttcctttt
ctnggttaat	ggactnggtn
ggcnnngtcc	gttcggttgg
600	
ggggancggn	nnt
613	

<210> 1084  
 <211> 886  
 <212> DNA  
 <213> Unknown (H38g934 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(886)  
 <223> n = A,T,C or G

<400> 1084	
ggtcccntcg	ngtatncntt
naccctctga	tgctgctcga
gcggccggca	gggtgatgga
60	
tatctgcaga	attcgccctt
ctgttacgca	ggaatatata
aaggggttac	tgaggaataa
120	
ataaatgggt	tactgaggaa
taaataaatg	ggttactgag
gaacaaatac	ataggggtga
180	
aagaactgta	aaatagaaaa
aggaccttnt	gctgctctc
aggatggcgg	nacttagggg
240	
ccatgtacat	gacgatgngg
ctgccnntna	agagtcccac
tnctcaneng	cctcagcccc
300	
ncttttttnt	cacnnncnt
ntttntctnc	cctcttnnnc
tcttttcttc	ctattccccc
360	
ccctcccnct	cctccctttt
gcntnaccat	tgncctnat
ccctttaatt	cnntcnntcn
420	
tctccctct	attccttcnn
tnttcgnttt	cantctctnc
ctctttctcc	cccnctttct
480	
ctctcttct	cttccctctg
tcatectngt	tenttctctt
ncctanttcc	ctctancctt
540	
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cctctcatct	cacntctctt
cctctctctn	tacttnnctc
600	
nnctcttctn	ctccgtctnc
cnctttctct	tctnnaagcc
acccctcnnn	cntnctctct
660	
ntctctctct	cactctctcc
tctccctnct	cntcactntt
ctccnctct	acntcctatn
720	
ctcncttct	nncttnactt
tgtaacgctc	tcctctctct
ctctacgcac	nttttatctc
780	
ttatctcnct	catcnccctc
mntctnca	netattnact
cttttctcnc	atactntatn
840	
ctcctntcnn	cttanatcnc
ctcccttctn	tnancnntc
actgcn	
886	

<210> 1085  
 <211> 125  
 <212> PRT

&lt;213&gt; Unknown (H38g1 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1          5          10          15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
      20          25          30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
      35          40          45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
      50          55          60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
 65          70          75          80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
      85          90          95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
      100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
      115          120          125

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&lt;210&gt; 1086

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g2 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1086

```

His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20          25          30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
      35          40          45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
      50          55          60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65          70          75          80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
      85          90          95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
      100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
      165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

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Met	Asp	Gly	Asp	Asn	Gln	Ser	Glu	Asn	Ser	Gln	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Ile	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Arg	Ile	Leu	Phe	Trp	Met	Phe	Leu
			20					25				30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Val	Leu	Ile	Ile	Leu	Ala
		35					40				45				
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro	Lys
65					70					75					80
Met	Leu	Val	Asn	Phe	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ser	Tyr	Ala	Gly
			85						90					95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Thr	Leu	Asp	Asn
			100					105					110		
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Thr	Cys	Cys
			115				120					125			
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Val	Leu	Leu
	130					135					140				
Leu	Ser	Leu	Cys	Trp	Gly	Leu	Ser	Val	Leu	Tyr	Gly	Leu	Leu	Leu	Thr
145					150					155					160
Phe	Leu	Leu	Thr	Arg	Val	Thr	Phe	Cys	Gly	Pro	Arg	Glu	Ile	His	Tyr
				165					170					175	
Leu	Phe	Cys	Asp	Met	Tyr	Ile	Leu	Leu	Trp	Leu	Ala	Cys	Ser	Asn	Thr
			180					185				190			
His	Ile	Ile	His	Thr	Ala	Leu	Ile	Ala	Thr	Gly	Cys	Phe	Ile	Phe	Leu
		195					200					205			
Thr	Pro	Leu	Gly	Phe	Met	Thr	Thr	Ser	Tyr	Val	Arg	Ile	Val	Arg	Thr
	210					215					220				
Ile	Leu	Gln	Met	Pro	Ser	Ala	Ser	Lys	Lys	Tyr	Lys	Thr	Phe	Ser	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Gly	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu	Ala
				245					250					255	
Met	Val	Tyr	Leu	Gln	Pro	Leu	His	Thr	Tyr	Ser	Met	Lys	Asp	Ser	Val
		260						265				270			



Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg Pro Lys  
 305 310

&lt;210&gt; 1088

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g4 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(305)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro  
 1 5 10 15  
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile  
 20 25 30  
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe  
 35 40 45  
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp  
 50 55 60  
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser  
 65 70 75 80  
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe  
 85 90 95  
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met  
 100 105 110  
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu  
 115 120 125  
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Pro Trp Leu  
 130 135 140  
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu  
 145 150 155 160  
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro  
 165 170 175  
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val  
 180 185 190  
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val  
 195 200 205  
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser  
 210 215 220  
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val  
 225 230 235 240  
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Tyr Leu Lys Ser  
 245 250 255  
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val  
 260 265 270  
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu  
 275 280 285  
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val  
 290 295 300  
 Cys  
 305

<210> 1089  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g5 protein)

<220>  
 <223> Synthetic construct

<400> 1089

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
          20          25          30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
          35          40          45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
65          70          75          80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
          85          90          95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
          100         105         110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
          115         120         125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
          130         135         140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
145         150         155         160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
          165         170         175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
          180         185         190
Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
          195         200         205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
          210         215         220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
225         230         235         240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
          245         250         255
Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
          260         265         270
Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
          275         280         285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
          290         295         300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
305         310         315

```

<210> 1090  
 <211> 342  
 <212> PRT  
 <213> Unknown (H38g6 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(342)  
 <223> Xaa = Any Amino Acid

<400> 1090  
 Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Ile Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met  
 35 40 45  
 Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe  
 145 150 155 160  
 Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met  
 165 170 175  
 Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser  
 180 185 190  
 Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn  
 195 200 205  
 Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr  
 210 215 220  
 Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser  
 225 230 235 240  
 Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser  
 245 250 255  
 Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser  
 260 265 270  
 Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr  
 275 280 285  
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn  
 290 295 300  
 Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa  
 305 310 315 320  
 Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys  
 325 330 335  
 Lys Gly Ser Lys Val Lys  
 340

<210> 1091

<211> 313

<212> PRT

<213> Unknown (H38g7 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1091

Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly

```

      1           5           10           15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20           25           30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu
      35           40           45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser
      50           55           60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys
      65           70           75           80
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala
      85           90           95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys
      100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn
      115          120          125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met
      130          135          140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr
      145          150          155          160
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His
      165          170          175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile
      180          185          190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu
      195          200          205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser
      210          215          220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr
      225          230          235          240
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
      245          250          255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
      260          265          270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe
      290          295          300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys
305          310

```

&lt;210&gt; 1092

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g8 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1092

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
  1           5           10           15
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
      20           25           30
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
      35           40           45
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
      50           55           60

```

```

Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
65          70          75          80
Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
85          90          95
Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
100        105        110
Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
115        120        125
Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
130        135        140
Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
145        150        155        160
Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
165        170        175
Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
180        185        190
Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
195        200        205
Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
210        215        220
Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
225        230        235        240
Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
245        250        255
Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
260        265        270
Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
275        280        285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
290        295        300
Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
305        310        315        320
Leu Ser Ser Lys Pro Lys Arg Arg
325

```

&lt;210&gt; 1093

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g9 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1093

```

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
1          5          10          15
Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
20        25        30
Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
35        40        45
Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
50        55        60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
65        70        75        80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
85        90        95
Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
100       105       110
Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
115       120       125
Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

```

```

      130              135              140
Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
145              150              155              160
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His
      165              170              175
Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr
      180              185              190
Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu
      195              200              205
Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
      210              215              220
Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
225              230              235              240
Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
      245              250              255
Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
      260              265              270
Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
      290              295              300
Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys
305              310              315

```

&lt;210&gt; 1094

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g10 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1094

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Thr Tyr Leu Ala Thr Val Leu Arg Asn Val Leu Asn
      35              40              45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
      50              55              60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Ser Tyr Ser Arg Val Ile Ser
      85              90              95
His Glu Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100              105              110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115              120              125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130              135              140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145              150              155              160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
      165              170              175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu Ala Cys
      180              185              190

```

```

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
    195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile
    210                215                220
Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
    225                230                235                240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
    245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
    260                265                270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
    275                280                285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
    290                295                300
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
    305                310                315                320
Phe Phe Leu Cys

```

&lt;210&gt; 1095

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g11 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1095

```

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
  1          5          10          15
Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
    20          25          30
Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
    35          40          45
Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
    50          55          60
Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
    65          70          75          80
Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
    85          90          95
Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
    100         105         110
Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
    115         120         125
Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
    130         135         140
Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
    145         150         155         160
Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
    165         170         175
Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
    180         185         190
Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
    195         200         205
Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
    210         215         220
Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
    225         230         235         240
Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
    245         250         255
Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

```

260 265 270  
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr  
 290 295 300  
 Cys Gln Ala Ser Arg Ser Asp  
 305 310

&lt;210&gt; 1096

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g12 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1096

Met Glu Gln Val Asn Lys Thr Val Val Arg Glu Phe Val Val Leu Gly  
 1 5 10 15  
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu  
 20 25 30  
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ser Thr  
 35 40 45  
 Ile Val Leu Asp Arg Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Val Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Phe Gly Ser Ser His Ser  
 100 105 110  
 Phe Leu Leu Ala Ala Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu  
 130 135 140  
 Met Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr  
 145 150 155 160  
 Ser Leu Val Phe His Leu Pro Phe His Ser Ser Asn Gln Leu His His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser  
 180 185 190  
 Gly Phe Ser Gln Leu Val Ile Phe Met Leu Gly Val Phe Ala Leu Val  
 195 200 205  
 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala  
 210 215 220  
 Ile Leu Lys Ile Pro Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ile Val Val Thr Val His Tyr Ser Cys Ala Ser  
 245 250 255  
 Phe Ile Tyr Leu Arg Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr  
 260 265 270  
 Leu Ile Ser Val Ser Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr  
 290 295 300  
 Ile Gly Gln Thr Phe Tyr Pro Leu Ser  
 305 310

&lt;210&gt; 1097

&lt;211&gt; 318

&lt;212&gt; PRT



&lt;213&gt; Unknown (H38g13 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1097

Cys	Val	Asp	Ser	Ser	Leu	Lys	Xaa	Glu	Ile	Thr	Gln	Xaa	Cys	Leu	Ser
1				5					10					15	
Leu	Leu	Leu	Xaa	Met	Ala	Glu	Gly	Trp	Arg	Leu	Tyr	Phe	Ile	Ile	Leu
			20					25					30		
Ile	Ile	Ser	Tyr	Lys	Phe	Cys	Thr	Leu	Leu	Gly	Asn	Val	Ile	Phe	Arg
		35					40					45			
Thr	Leu	Val	Cys	Ser	Leu	Gly	Phe	His	Thr	Ser	Cys	Met	Tyr	Phe	Phe
	50					55					60				
Pro	Xaa	Lys	Ile	Ser	Leu	Xaa	Leu	Ala	Xaa	Val	Cys	His	Ser	Ile	Ile
65					70				75					80	
Ala	Leu	Pro	Ser	Thr	Gln	Lys	Xaa	Ala	Ile	Asn	Val	Gln	Gly	Ala	Ala
				85					90					95	
Val	His	Val	Phe	Ser	Phe	Pro	Cys	Leu	Tyr	Cys	Pro	Glu	Ile	Phe	Leu
			100					105					110		
His	Ser	Leu	Thr	Gln	Cys	His	Pro	Phe	Ile	Ala	Ile	Gly	Tyr	Pro	Leu
		115					120					125			
Gln	Gly	Met	His	Thr	Ile	Thr	His	Lys	Leu	Tyr	Ile	Leu	Leu	Thr	Thr
		130				135					140				
Gly	Pro	Trp	Arg	Gly	Cys	Xaa	Leu	His	Val	Asn	Leu	Leu	Thr	Ala	Ile
145					150					155					160
Leu	Gly	Ser	Tyr	Pro	Asn	Pro	Val	Pro	Thr	Lys	Leu	Trp	Leu	Ser	Phe
				165					170					175	
Pro	Ser	Ile	Pro	Glu	Val	Lys	Leu	Xaa	Pro	Met	Gln	Ala	Tyr	Thr	Lys
			180					185					190		
Pro	Tyr	Ala	Gly	Leu	Ser	Leu	Cys	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser
		195					200					205			
Phe	Ser	Leu	Phe	Ser	Ile	Ile	Ser	Ile	Ser	Tyr	Ile	Cys	Asn	Glu	Ile
		210				215					220				
Asp	Ile	Pro	Lys	Ile	Ile	Ser	Ala	Asp	Ser	Val	His	Gly	Ala	Phe	Ser
225					230					235					240
Thr	Cys	Leu	Ala	His	Leu	Phe	Ala	Phe	Ser	Thr	Cys	Ile	Ala	Gln	Pro
				245					250					255	
Ala	Val	Cys	Asn	Ser	Leu	Trp	Pro	Trp	Thr	Glu	Ala	Gln	Thr	Glu	Ser
			260					265					270		
Ser	Arg	Asp	Ser	Val	Ile	Gln	Arg	Pro	Asn	Leu	Cys	Val	Thr	Ile	Ser
		275					280					285			
Leu	Asn	Ser	Leu	Ile	Ser	Ser	Leu	Arg	Asn	Glu	Ser	Val	Lys	Gln	Ala
	290					295					300				
Ser	His	Lys	Ile	Phe	Lys	Glu	Gln	Thr	Leu	Phe	Met	Lys	Ile		
305					310					315					

&lt;210&gt; 1098

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g14 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
          20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
          65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
          145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
          210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
          225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
          290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
          305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

```

<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15

```

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
      50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys
      100     105     110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115     120     125
Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130     135     140
Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln
      145     150     155     160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165     170     175
Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
      180     185     190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
      195     200     205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
      210     215     220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225     230     235     240
Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245     250     255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260     265     270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
      275     280     285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290     295     300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
      305     310     315     320
Phe Ser

```

&lt;210&gt; 1100

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g16 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1100

```

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
  1      5      10      15
Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      20      25      30
Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
      35      40      45
Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
      50      55      60
Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
      65      70      75      80
Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu

```

```

      85              90              95
His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr
      100              105              110
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu
      115              120              125
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe
      130              135              140
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu
145              150              155              160
Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
      165              170              175
Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
      180              185              190
Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
      195              200              205
Ser His Leu Ala Val Val Leu Phe Tyr Gly Thr Ile Met Ser Pro
      210              215              220
Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
225              230              235              240
Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
      245              250              255
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
      260              265              270
Val Lys Phe Phe Ser Val Gln
      275

```

&lt;210&gt; 1101

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g17 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(257)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1101

```

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu
 1              5              10              15
Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His
      20              25              30
Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys
      35              40              45
Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys
      50              55              60
His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu
65              70              75              80
Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser
      85              90              95
Leu Ala Val Gln Leu Pro Leu Gly Gly Asn Lys Val Asp Asp Phe Leu
      100              105              110
Cys Glu Val Ser Ala Met Ile Lys Ile Ser Arg Phe Asp Thr Thr Phe
      115              120              125
Asn Val Ser Met Leu Ser Ile Val Arg Ile Phe Xaa Ser Leu Val Leu
      130              135              140
Xaa Ser Ile Ile Phe Ala Tyr Cys Gly Phe Ile Val Ala Thr Val Leu
145              150              155              160
Arg Ile Gln Ser Ser Gly Gly Lys Lys Glu Val Phe Asn Thr Cys Gly
      165              170              175

```

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val  
 180 185 190  
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe  
 195 200 205  
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser  
 210 215 220  
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr  
 225 230 235 240  
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe  
 245 250 255  
 Ile

&lt;210&gt; 1102

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g18 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu  
 1 5 10 15  
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro  
 65 70 75 80  
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu  
 100 105 110  
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe  
 130 135 140  
 Leu Leu Leu Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu  
 145 150 155 160  
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile  
 165 170 175  
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys  
 180 185 190  
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe  
 195 200 205  
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val  
 210 215 220  
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr  
 245 250 255  
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys  
 260 265 270  
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

275	280	285
Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg		
290	295	300
Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser		
305	310	315
Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys		
325	330	

&lt;210&gt; 1103

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g19 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1103

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly		
1	5	10
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser		
20	25	30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser		
35	40	45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala		
50	55	60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys		
65	70	75
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly		
85	90	95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met		
100	105	110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys		
115	120	125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe		
130	135	140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu		
145	150	155
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser		
165	170	175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr		
180	185	190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val		
195	200	205
Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr		
210	215	220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu		
225	230	235
Ser Ala His Ser Thr Ala Val Leu Leu Phe Gly Pro Pro Met Phe		
245	250	255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala		
260	265	270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr		
275	280	285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln		
290	295	300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu		
305	310	315
		320

Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr  
 325 330

<210> 1104

<211> 339

<212> PRT

<213> Unknown (H38g20 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 1104

Asp	Thr	Asp	Pro	Gln	Ser	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5					10					15	
Glu	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ile	Ile	Leu
		35				40						45			
Ala	Ile	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Phe	Pro	Asp	Ser	Arg	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70					75					80
Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Asp	Met	Glu
			100					105					110		
Glu	Asn	Met	Phe	Leu	Ser	Val	Val	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile
		115				120						125			
Cys	His	Pro	Leu	Tyr	Arg	Ser	Ala	Ile	Leu	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Asp	Ser	Leu	Ser	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Ser	Leu
145					150				155						160
Leu	Asp	Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe
				165					170					175	
Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Pro
			180					185					190		
His	Leu	Ala	Cys	Cys	Asp	Ile	Phe	Thr	Arg	Asn	Ile	Asn	Leu	Tyr	Phe
		195				200						205			
Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser
	210				215						220				
Tyr	Tyr	Lys	Ile	Val	Ser	Phe	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly
225				230						235					240
Lys	Tyr	Lys	Ala	Phe	Ser	Ala	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Tyr
			245						250					255	
Xaa	Val	Tyr	Gly	Thr	Gly	Phe	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser
			260					265					270		
Ser	Ser	Pro	Arg	Lys	Gly	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val
		275					280					285			
Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Gly	Asp	Ile
	290					295					300				
Lys	Ser	Val	Leu	Arg	Gln	Pro	His	Gly	Ser	Thr	Val	Xaa	Ser	Gln	Tyr
305					310					315					320
Leu	Leu	Ile	Cys	Ser	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser
				325					330					335	
Lys	Val	Lys													

<210> 1105  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g21 protein)

<220>  
 <223> Synthetic construct

<400> 1105

```

Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly
 1          5          10          15
Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Leu Cys Leu
          20          25          30
Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile
          35          40          45
Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
          50          55          60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro
          65          70          75          80
Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
          85          90          95
Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys
          100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met
          130          135          140
Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr
          145          150          155          160
Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His
          165          170          175
Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile
          180          185          190
Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val
          195          200          205
Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser
          210          215          220
Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
          225          230          235          240
Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu
          245          250          255
Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu
          260          265          270
Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val
          290          295          300
Leu Ser Arg His Leu His Leu Leu Lys Met
          305          310

```

<210> 1106  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g22 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid



&lt;400&gt; 1106

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1           5           10           15
Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
          20           25           30
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr
          35           40           45
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
          50           55           60
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
          65           70           75           80
Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
          85           90           95
Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
          100          105          110
Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
          130          135          140
Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
          145          150          155          160
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
          165          170          175
Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
          180          185          190
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
          195          200          205
Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
          210          215          220
Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
          225          230          235          240
His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
          245          250          255
Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
          260          265          270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
          275          280          285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
          290          295          300
Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
          305          310          315

```

&lt;210&gt; 1107

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g23 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1107

```

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro
 1           5           10           15
His Thr Glu Gly Leu Glu Thr Ile Leu Val Leu Phe Leu Ser Phe
          20           25           30
Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

```

	35					40				45					
Ser	Ser	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Cys	Lys	Leu
	50					55					60				
Ser	Val	Phe	Asp	Leu	Phe	Phe	Pro	Ser	Val	Ser	Ser	Pro	Lys	Met	Leu
65					70					75					80
Cys	Tyr	Leu	Ser	Gly	Asn	Ser	Arg	Ala	Ile	Ser	Tyr	Ala	Gly	Cys	Ala
				85					90					95	
Ser	Gln	Leu	Phe	Tyr	His	Phe	Leu	Gly	Cys	Thr	Glu	Cys	Phe	Leu	
		100					105					110			
Tyr	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
		115					120					125			
Arg	Tyr	Thr	Ile	Ile	Met	Ser	His	Arg	Ala	Cys	Ile	Ile	Leu	Ala	Met
	130					135					140				
Gly	Thr	Ser	Phe	Phe	Gly	Cys	Ile	Gln	Ala	Thr	Phe	Leu	Thr	Thr	Leu
145					150					155					160
Thr	Phe	Gln	Leu	Pro	Tyr	Cys	Val	Pro	Asn	Glu	Val	Asp	Tyr	Tyr	Phe
				165					170					175	
Cys	Asp	Ile	Pro	Val	Met	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	Ser	Ala
			180					185					190		
Leu	Glu	Met	Val	Gly	Phe	Ile	Ser	Val	Gly	Leu	Met	Pro	Leu	Ser	Cys
	195						200					205			
Phe	Leu	Ile	Leu	Thr	Ser	Tyr	Ser	Gly	Ile	Val	Phe	Ser	Ile	Leu	
	210					215				220					
Xaa	Ile	Cys	Ser	Ala	Glu	Gly	Arg	Arg	Arg	Ala	Phe	Ser	Thr	Cys	Ser
225					230					235					240
Ala	His	Leu	Thr	Ala	Ile	Leu	Leu	Phe	Tyr	Met	Pro	Val	Val	Leu	Ile
				245					250					255	
Tyr	Leu	Arg	Pro	Thr	His	Ser	Leu	Trp	Leu	Asp	Ala	Thr	Val	Gln	Ile
			260					265					270		
Leu	Asn	Asn	Leu	Val	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu
	275						280					285			
Arg	Asn	Lys	Glu	Val	Lys	Leu	Ser	Leu	Arg	Lys	Val	Leu	Tyr	Gln	Leu
	290					295					300				
Gly	Phe	Leu	Pro	Glu	Gln	Leu									
305					310										

&lt;210&gt; 1108

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g24 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1108

Met	Asp	Ile	Pro	Gln	Asn	Ile	Thr	Glu	Phe	Phe	Met	Leu	Gly	Leu	Ser
1				5					10					15	
Gln	Asn	Ser	Glu	Val	Gln	Arg	Val	Leu	Phe	Val	Val	Phe	Leu	Leu	Ile
			20					25					30		
Tyr	Val	Val	Thr	Val	Cys	Gly	Asn	Met	Leu	Ile	Val	Val	Thr	Ile	Thr
		35					40					45			
Ser	Ser	Pro	Thr	Leu	Ala	Ser	Pro	Val	Tyr	Phe	Phe	Leu	Ala	Asn	Leu
	50					55					60				
Ser	Phe	Ile	Asp	Thr	Phe	Tyr	Ser	Ser	Ser	Met	Ala	Pro	Lys	Leu	Ile
65					70					75					80
Ala	Asp	Ser	Leu	Tyr	Glu	Gly	Arg	Thr	Ile	Ser	Tyr	Glu	Cys	Cys	Met
				85					90					95	
Ala	Gln	Leu	Phe	Gly	Ala	His	Phe	Leu	Gly	Gly	Val	Glu	Ile	Ile	Leu
			100					105					110		
Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu
		115					120					125			

```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
  130                135                140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
 145                150                155                160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
 165                170                175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
 180                185                190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
 195                200                205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
 210                215                220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
 225                230                235                240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
 245                250                255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
 260                265                270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275                280                285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
 290                295                300

```

&lt;210&gt; 1109

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g25 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
  1                5                10                15
Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
 20                25                30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
 35                40                45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
 50                55                60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
 65                70                75                80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
 85                90                95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
100                105                110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
115                120                125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
130                135                140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
145                150                155                160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
165                170                175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
180                185                190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
195                200                205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
210                215                220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```

225                      230                      235                      240  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala  
                                  245                      250                      255  
 Val Lys Lys Ile Leu His Gln Thr Ala Cys  
                                  260                      265

&lt;210&gt; 1110

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g26 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1110

Met Gly Asn Ser Asn Gln Ser Phe Met Thr Glu Phe Val Leu Leu Gly  
 1                      5                      10                      15  
 Leu Ser Gly Tyr Pro Glu Leu Glu Ala Ile Tyr Phe Val Leu Val Leu  
                                  20                      25                      30  
 Cys Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Ile Ile Ile Val  
                                  35                      40                      45  
 Ser Val Tyr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
                                  50                      55                      60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Leu  
 65                      70                      75                      80  
 Phe Leu Ser Ser Phe Leu Thr Ser Lys Lys Thr Ile Ser Phe Ser Gly  
                                  85                      90                      95  
 Cys Gly Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys  
                                  100                      105                      110  
 Val Leu Leu Ser Met Met Ala Phe Asp Cys Tyr Val Ala Ile Cys Asn  
                                  115                      120                      125  
 Pro Leu Xaa Tyr Pro Ile Ile Met Ser Lys Ala Ser Tyr Met Ser Met  
                                  130                      135                      140  
 Ala Ala Gly Ser Trp Ile Gly Gly Gly Ile Asn Ser Val Leu Gln Thr  
 145                      150                      155                      160  
 Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His  
                                  165                      170                      175  
 Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asn Ile  
                                  180                      185                      190  
 Ser Ile Asn Ile Ile Ser Met Val Val Ala Ser Met Ile Phe Leu Val  
                                  195                      200                      205  
 Gly Pro Val Leu Phe Ile Phe Val Thr Tyr Val Phe Ile Leu Ser Thr  
                                  210                      215                      220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Ala Ser Ser Thr  
 225                      230                      235                      240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Arg Thr Ile Leu  
                                  245                      250                      255  
 Phe Met Tyr Ala Lys Pro Lys Ala Lys Asp Ser Ser Gly Ala Asp Lys  
                                  260                      265                      270  
 Glu Gln Val Thr Asp Lys Ile Ile Ser Leu Phe Tyr Gly Val Val Thr  
                                  275                      280                      285  
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
                                  290                      295                      300  
 Ala Ala Val Lys Ser Ile Leu Xaa Gln Lys Cys Phe Leu Glu  
 305                      310                      315

&lt;210&gt; 1111

<211> 329  
 <212> PRT  
 <213> Unknown (H38g27 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(329)  
 <223> Xaa = Any Amino Acid

<400> 1111

```

Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu
 20          25          30
Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile
 35          40          45
Ile Phe Ile Ser Pro Ala Leu Gly Ser Pro Met Tyr Ser Phe Pro Ser
 50          55          60
Tyr Leu Phe Ile Ile Asp Ile Phe Cys Ser Ser Ser Ile Ala Pro Lys
 65          70          75          80
Met Asn Phe Asp Leu Ile Ser Glu Lys Asn Thr Ile Ser Phe Asn Gly
 85          90          95
Cys Met Thr Gln Leu Phe Thr Glu His Phe Phe Thr Glu His Phe Phe
 100         105         110
Glu Ala Ala Glu Ile Ile Leu Leu Ser Val Met Ala Tyr Asp His Tyr
 115         120         125
Val Ala Ile Arg Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 130         135         140
Met Cys Gly Phe Leu Met Val Val Ala Gly Ile Leu Gly Phe Val His
 145         150         155         160
Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
 165         170         175
Asn Val Ile Asn His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 180         185         190
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 195         200         205
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 210         215         220
Ile Ile Leu Cys Phe Leu Arg Thr His Ser Ser Glu Gly Arg Arg Lys
 225         230         235         240
Ala Leu Ser Ser Cys Ala Ser His Ile Phe Ile Val Ile Leu Phe Phe
 245         250         255
Val Pro Phe Ser Tyr Leu Tyr Leu Arg Pro Ile His Ser Phe Pro Thr
 260         265         270
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu Asn
 275         280         285
Pro Leu Ile Tyr Thr Leu Lys Asn Lys Glu Val Lys Asn Val Ile Lys
 290         295         300
Lys Leu Trp Lys Gln Ile Met Thr Thr Asp Asp Lys Xaa Val Leu Xaa
 305         310         315         320
His Lys His Leu Gly Lys Asn Ile Trp
 325

```

<210> 1112  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g28 protein)

<220>

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1           5           10           15
Leu Ser Gly His Pro Arg Leu Glu Leu Phe Phe Val Leu Ile Phe
 20           25           30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35           40           45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65           70           75
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85           90           95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
100           105           110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
115           120           125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
130           135           140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
145           150           155
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
165           170           175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
180           185           190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
195           200           205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
210           215           220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
225           230           235
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
245           250           255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
260           265           270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
275           280           285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
290           295           300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
305           310           315

```

## &lt;210&gt; 1113

## &lt;211&gt; 264

## &lt;212&gt; PRT

## &lt;213&gt; Unknown (H38g29 protein)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1           5           10           15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
 20           25           30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu
 35           40           45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
 50           55           60

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met  
 65 70 75 80  
 Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile  
 85 90 95  
 Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val  
 100 105 110  
 Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu  
 115 120 125  
 Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe  
 130 135 140  
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe  
 145 150 155 160  
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu  
 165 170 175  
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser  
 180 185 190  
 Thr Cys Ala Phe His Ile Thr Val Val Leu Phe Phe Val Pro Cys  
 195 200 205  
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala  
 210 215 220  
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile  
 225 230 235 240  
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp  
 245 250 255  
 Ser Gln Ile Ile Trp Gly Asn Asn  
 260

&lt;210&gt; 1114

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g30 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1114

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15  
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val  
 20 25 30  
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys  
 35 40 45  
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu  
 50 55 60  
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met  
 65 70 75 80  
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe  
 85 90 95  
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser  
 100 105 110  
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu  
 115 120 125  
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val  
 130 135 140  
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg  
 145 150 155 160  
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe  
 165 170 175  
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe  
 180 185 190  
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

      195              200              205
Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
  210              215              220
Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
  225              230              235              240
Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
      245              250              255
Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
      260              265              270
Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
      275              280              285
Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
      290              295              300
Leu Ser Lys His Arg Phe Ser Arg
305              310

```

&lt;210&gt; 1115

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g31 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(285)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1115

```

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly
      85              90              95
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp
      100              105              110
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys
      115              120              125
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu
      130              135              140
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145              150              155              160
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser
      165              170              175
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp
      180              185              190
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly
      195              200              205
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe
      210              215              220
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser
      225              230              235              240
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255

```



Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp  
                   260                  265                  270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro  
                   275                  280                  285

<210> 1116

<211> 317

<212> PRT

<213> Unknown (H38g32 protein)

<220>

<223> Synthetic construct

<400> 1116

Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly  
 1                  5                  10                  15  
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu  
                   20                  25                  30  
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala  
                   35                  40                  45  
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly  
                   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Val Pro Ser  
 65                  70                  75                  80  
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly  
                   85                  90                  95  
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys  
                   100                  105                  110  
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
                   115                  120                  125  
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met  
                   130                  135                  140  
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr  
 145                  150                  155                  160  
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His  
                   165                  170                  175  
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile  
                   180                  185                  190  
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val  
                   195                  200                  205  
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr  
                   210                  215                  220  
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr  
 225                  230                  235                  240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe  
                   245                  250                  255  
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys  
                   260                  265                  270  
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr  
                   275                  280                  285  
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys  
                   290                  295                  300  
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His  
 305                  310                  315

<210> 1117

<211> 309

<212> PRT

<213> Unknown (H38g33 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1117

```

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1           5           10           15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
          20           25           30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
          35           40           45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
          50           55           60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
          65           70           75           80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
          85           90           95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
          100          105          110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
          115          120          125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
          130          135          140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
          145          150          155          160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
          165          170          175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
          180          185          190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
          195          200          205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
          210          215          220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
          225          230          235          240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
          245          250          255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
          260          265          270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
          275          280          285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
          290          295          300
Ser Leu Gly Glu Lys
          305

```

&lt;210&gt; 1118

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g34 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
 1           5           10           15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
          20           25           30

```

Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr  
           35                                  40                                  45  
 Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Cys Phe Leu  
           50                                  55                                  60  
 Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr  
   65                                  70                                  75                                  80  
 Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala  
                                   85                                  90                                  95  
 Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu  
                                   100                                  105                                  110  
 Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His  
                                   115                                  120                                  125  
 Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile  
                                   130                                  135                                  140  
 Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile  
   145                                  150                                  155                                  160  
 Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His  
                                   165                                  170                                  175  
 Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile  
                                   180                                  185                                  190  
 Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe  
                                   195                                  200                                  205  
 Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr  
                                   210                                  215                                  220  
 Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met  
   225                                  230                                  235                                  240  
 Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile  
                                   245                                  250                                  255  
 Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val  
                                   260                                  265                                  270  
 His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn  
                                   275                                  280                                  285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val  
                                   290                                  295                                  300  
 Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe  
   305                                  310                                  315                                  320  
 Cys Asp Leu His Asp Phe Trp Ala Phe  
                                   325

&lt;210&gt; 1119

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g35 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1119

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met  
   1                                  5                                  10                                  15  
 Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His  
                                   20                                  25                                  30  
 Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu  
                                   35                                  40                                  45  
 Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg  
                                   50                                  55                                  60  
 Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr  
   65                                  70                                  75                                  80  
 Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Leu Thr Val Met Ser Tyr  
                                   85                                  90                                  95  
 Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met

			100					105					110				
Arg	Pro	Tyr	Val	Cys	Ile	Gly	Thr	Val	Val	Phe	Ser	Trp	Val	Gly	Gly		
		115					120					125					
Phe	Leu	Ser	Val	Leu	Phe	Pro	Thr	Ile	Leu	Ile	Ser	Gln	Leu	Pro	Phe		
	130					135					140						
Cys	Gly	Ser	Asn	Ile	Ile	Asn	His	Phe	Phe	Cys	Asp	Ser	Gly	Pro	Leu		
145				150						155					160		
Leu	Ala	Leu	Ala	Cys	Ala	Asp	Thr	Thr	Ala	Ile	Glu	Leu	Met	Asp	Phe		
			165						170					175			
Met	Leu	Ser	Ser	Met	Val	Ile	Leu	Cys	Cys	Ile	Val	Leu	Val	Ala	Tyr		
		180						185				190					
Ser	Tyr	Thr	Tyr	Ile	Ile	Leu	Thr	Ile	Met	Arg	Ile	Pro	Ser	Ala	Ser		
	195						200					205					
Gly	Arg	Lys	Lys	Ala	Phe	Asn	Thr	Cys	Ala	Ser	His	Leu	Thr	Ile	Val		
	210					215					220						
Ile	Ile	Ser	Ser	Gly	Ile	Thr	Val	Phe	Ile	Tyr	Val	Thr	Pro	Ser	Gln		
225				230						235					240		
Lys	Glu	Tyr	Leu	Glu	Ile	Asn	Lys	Ile	Pro	Ser	Val	Leu	Ser	Ser	Leu		
			245					250				255					
Val	Thr	Pro	Phe	Leu	Asn	Pro	Phe	Ile	Tyr	Thr	Leu	Arg	Asn	Asp	Thr		
		260					265					270					
Val	Gln	Gly	Val	Leu	Arg	Asp	Val	Trp	Val	Arg	Val	Arg	Gly	Val	Phe		
	275					280						285					
Glu	Lys	Arg	Met	Arg	Ala	Val	Leu										
	290					295											

&lt;210&gt; 1120

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g36 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1120

Met	Trp	Tyr	Asn	Asn	Ser	Ala	Gly	Pro	Phe	Leu	Leu	Thr	Gly	Phe	Leu		
1			5					10					15				
Gly	Ser	Glu	Ala	Val	His	Tyr	Arg	Ile	Ser	Met	Ser	Phe	Phe	Val	Ile		
		20					25					30					
Tyr	Phe	Ser	Val	Leu	Phe	Gly	Asn	Gly	Thr	Leu	Leu	Val	Leu	Ile	Trp		
	35					40						45					
Asn	Asp	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	Leu	Ala	Met	Leu		
	50					55					60						
Ala	Asp	Thr	Asp	Leu	Gly	Met	Thr	Phe	Thr	Thr	Met	Pro	Thr	Val	Leu		
65				70						75					80		
Gly	Val	Leu	Leu	Leu	Asp	Gln	Arg	Glu	Ile	Ala	His	Ala	Ala	Cys	Phe		
			85					90				95					
Thr	Gln	Ser	Phe	Ile	His	Ser	Leu	Ala	Ile	Val	Glu	Ser	Gly	Ile	Leu		
		100					105					110					
Leu	Val	Leu	Ala	Tyr	Asp	Cys	Phe	Ile	Ala	Ile	Arg	Thr	Pro	Leu	Arg		
	115					120						125					
Tyr	Asn	Cys	Ile	Leu	Thr	Asn	Ser	Arg	Val	Met	Asn	Ile	Gly	Leu	Gly		
	130					135					140						
Val	Leu	Met	Arg	Gly	Phe	Met	Ser	Ile	Leu	Pro	Ile	Ile	Leu	Ser	Leu		
145				150						155					160		
Tyr	Cys	Tyr	Pro	Tyr	Cys	Gly	Ser	Arg	Ala	Leu	Leu	His	Thr	Phe	Cys		
			165					170						175			
Leu	His	Gln	Asp	Val	Ile	Lys	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Phe	Asn		
		180					185					190					
His	Ile	Tyr	Pro	Ile	Ile	Gln	Thr	Ser	Leu	Thr	Val	Phe	Leu	Asp	Ala		
	195					200						205					

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly
  210                      215                      220
Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser
225                      230                      235                      240
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser
                      245                      250                      255
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr
                      260                      265                      270
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile
                      275                      280                      285
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe
                      290                      295                      300
Ser Gly Gln Ser Arg Ala
305                      310

```

<210> 1121  
 <211> 332  
 <212> PRT  
 <213> Unknown (H38g37 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(332)  
 <223> Xaa = Any Amino Acid

```

<400> 1121
His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1                      5                      10                      15
Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                      20                      25                      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile
                      35                      40                      45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
                      50                      55                      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65                      70                      75                      80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser
                      85                      90                      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys
                      100                     105                     110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
                      115                     120                     125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys
                      130                     135                     140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                     150                     155                     160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu
                      165                     170                     175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                      180                     185                     190
Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
                      195                     200                     205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
                      210                     215                     220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                     230                     235                     240
Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg
                      245                     250                     255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

			260					265				270					
Asn	Gly	Val	Val	Ala	Ser	Leu	Ile	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu		
		275					280					285					
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu		
	290					295					300						
Arg	Arg	Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro		
305					310						315				320		
Phe	Ser	Trp	Trp	Val	Arg	Lys	Gly	Asn	His	Ile	Lys						
				325					330								

&lt;210&gt; 1122

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g38 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1122

Met	Gly	Asp	Asn	Ile	Thr	Ser	Ile	Arg	Glu	Phe	Leu	Leu	Leu	Gly	Phe		
1			5					10						15			
Pro	Val	Gly	Pro	Arg	Ile	Gln	Met	Leu	Leu	Phe	Gly	Leu	Phe	Ser	Leu		
			20					25					30				
Phe	Tyr	Val	Phe	Thr	Leu	Leu	Gly	Asn	Gly	Thr	Ile	Leu	Gly	Leu	Ile		
		35					40					45					
Ser	Leu	Asp	Ser	Arg	Leu	His	Ala	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His		
	50					55					60						
Leu	Ala	Val	Val	Asp	Ile	Ala	Tyr	Ala	Cys	Asn	Thr	Val	Pro	Arg	Met		
65					70				75					80			
Leu	Val	Asn	Leu	Leu	His	Pro	Ala	Lys	Pro	Ile	Ser	Phe	Ala	Gly	Arg		
			85						90					95			
Met	Met	Gln	Thr	Phe	Leu	Phe	Ser	Thr	Phe	Ala	Val	Thr	Glu	Cys	Leu		
			100					105					110				
Leu	Leu	Val	Val	Met	Ser	Tyr	Asp	Leu	Tyr	Val	Ala	Ile	Cys	His	Pro		
	115						120					125					
Leu	Arg	Tyr	Leu	Ala	Ile	Met	Thr	Trp	Arg	Val	Cys	Ile	Thr	Leu	Ala		
	130					135					140						
Val	Thr	Ser	Trp	Thr	Thr	Gly	Val	Leu	Leu	Ser	Leu	Ile	His	Leu	Val		
145					150					155					160		
Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Arg	Pro	Gln	Lys	Ile	Tyr	His	Phe		
			165						170					175			
Phe	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	His		
		180						185					190				
Ile	Asn	Glu	Asn	Met	Val	Leu	Ala	Gly	Ala	Ile	Ser	Gly	Leu	Val	Gly		
	195					200						205					
Pro	Leu	Ser	Thr	Ile	Val	Val	Ser	Tyr	Met	Cys	Ile	Leu	Cys	Ala	Ile		
	210					215					220						
Leu	Gln	Ile	Gln	Ser	Arg	Glu	Val	Gln	Arg	Lys	Ala	Phe	Arg	Thr	Cys		
225					230					235					240		
Phe	Ser	His	Leu	Cys	Val	Ile	Gly	Leu	Val	Tyr	Gly	Thr	Ala	Ile	Ile		
			245						250					255			
Met	Tyr	Val	Gly	Pro	Arg	Tyr	Gly	Asn	Pro	Lys	Glu	Gln	Lys	Lys	Tyr		
		260						265					270				
Leu	Leu	Leu	Phe	His	Ser	Leu	Phe	Asn	Pro	Met	Leu	Asn	Pro	Leu	Ile		
		275					280					285					
Cys	Ser	Leu	Arg	Asn	Ser	Glu	Val	Lys	Asn	Thr	Leu	Lys	Arg	Val	Leu		
	290					295					300						
Gly	Val	Glu	Arg	Ala	Leu												
305					310												

&lt;210&gt; 1123

<211> 323  
 <212> PRT  
 <213> Unknown (H38g39 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

<400> 1123  
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu  
 50 55 60  
 Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly  
 195 200 205  
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210 215 220  
 Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly  
 245 250 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly  
 260 265 270  
 Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg  
 290 295 300  
 Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe  
 305 310 315 320  
 Leu Cys Leu

<210> 1124  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20          25          30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Val Ser Ser Asp Pro His Leu His Thr Pro Met Cys Phe Phe Leu
 50          55          60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Met Gln Ser His Thr Arg Val Ile Ser Tyr Glu
 85          90          95
Gly Cys Leu Thr Arg Ile Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100         105         110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115         120         125
Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130         135         140
Phe Leu Leu Val Tyr Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145         150         155         160
Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile Ser
 165         170         175
Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp
 180         185         190
Ser Val Ile Asn Ser Ile Phe Met Tyr Phe His Ser Thr Met Phe Gly
 195         200         205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210         215         220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225         230         235         240
Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr Gly
 245         250         255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly
 260         265         270
Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu
 275         280         285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg
 290         295         300
Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305         310         315         320

```

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125



```

Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115          120          125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn
 145          150          155          160
Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn
 165          170          175
Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr
 180          185          190
Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
 195          200          205
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser
 210          215          220
Ile Leu Arg Val Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His
 225          230          235          240
Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu
 245          250          255
Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val
 260          265          270
Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu
 275          280          285
Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr
 290          295          300
Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp
 305          310          315          320
Val Lys Lys Gly Ser Lys Val
 325

```

&lt;210&gt; 1126

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g42 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1126

```

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro
 1          5          10          15
Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr
 20          25          30
Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp
 35          40          45
Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50          55          60
Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

65					70					75					80
Ala	Cys	Leu	Leu	Gly	Glu	Glu	Lys	Thr	Ile	Ser	Phe	Ala	Gly	Cys	Met
				85					90					95	
Ile	Gln	Thr	Tyr	Phe	Tyr	Phe	Phe	Leu	Gly	Thr	Val	Glu	Phe	Ile	Leu
			100					105					110		
Leu	Ala	Val	Met	Ser	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asp	Pro	Leu
			115				120					125			
His	Tyr	Thr	Val	Ile	Met	Asn	Ser	Arg	Ala	Cys	Leu	Leu	Val	Leu	
			130			135					140				
Gly	Cys	Trp	Val	Gly	Ala	Phe	Leu	Ser	Val	Leu	Phe	Pro	Thr	Ile	Val
				150						155					160
Val	Thr	Arg	Leu	Pro	Tyr	Cys	Arg	Lys	Glu	Ile	Asn	His	Phe	Phe	Cys
				165					170					175	
Asp	Ile	Ala	Pro	Leu	Leu	Gln	Val	Ala	Cys	Ile	Asn	Thr	His	Leu	Ile
			180					185					190		
Glu	Lys	Ile	Asn	Phe	Leu	Leu	Ser	Ala	Leu	Val	Ile	Leu	Ser	Ser	Leu
			195				200					205			
Ala	Phe	Thr	Thr	Gly	Ser	Tyr	Val	Tyr	Ile	Ile	Ser	Thr	Ile	Leu	Arg
			210			215					220				
Ile	Pro	Ser	Thr	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser
				230					235					240	
His	Ile	Thr	Val	Val	Ser	Ile	Ala	His	Gly	Ser	Asn	Ile	Phe	Val	Tyr
				245					250					255	
Val	Arg	Pro	Asn	Gln	Asn	Ser	Ser	Leu	Asp	Tyr	Asp	Lys	Val	Ala	Ala
			260					265					270		
Val	Leu	Ile	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Ile	Tyr	Ser
			275				280					285			
Leu	Arg	Asn	Glu	Lys	Val	Gln	Glu	Val	Leu	Arg	Glu	Thr	Val	Asn	Arg
			290			295					300				
Ile	Met	Thr	Leu	Ile	Gln	Arg	Lys	Thr							
			305			310									

&lt;210&gt; 1127

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g43 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(247)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1127

Met	Gly	Asn	Ile	Asn	Ile	Ser	Leu	Glu	Asn	Tyr	Phe	Ile	Leu	Leu	Gly
1				5				10						15	
Leu	Ser	Asn	Xaa	Pro	Pro	Leu	Glu	Ile	Val	Ile	Phe	Val	Val	Leu	Leu
			20					25					30		
Ile	Phe	Cys	Phe	Met	Thr	Leu	Ile	Gly	Lys	Leu	Phe	Ser	Ile	Ile	Leu
			35				40					45			
Ser	Tyr	Leu	Asp	Ser	His	Pro	His	Thr	Pro	Arg	Tyr	Leu	Phe	Ser	Phe
			50			55					60				
Leu	Asp	Phe	Cys	Tyr	Thr	Ile	Ser	Ser	Ile	Phe	Xaa	Leu	Gln	Tyr	Asn
					70					75					80
Leu	Trp	Gly	Pro	Gln	Lys	Asn	Ile	Ser	Tyr	Ala	Ser	Gly	Met	Ile	Gln
				85					90					95	
Ile	Tyr	Phe	Val	Leu	Thr	Leu	Gly	Thr	Met	Asp	Cys	Ala	Leu	Leu	Val
			100					105					110		
Val	Met	Ser	Arg	Thr	Val	Tyr	Ala	Gly	His	Arg	His	Leu	Pro	Tyr	
			115				120					125			

```

Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
 130                135                140
Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145                150                155                160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
                165                170                175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
                180                185                190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
                195                200                205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
                210                215                220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225                230                235                240
Arg Pro Ile Leu Gly Asn Ser
                245

```

&lt;210&gt; 1128

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g44 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
 1                5                10                15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
                20                25                30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
                35                40                45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
                50                55                60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65                70                75                80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
                85                90                95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
                100                105                110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
                115                120                125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
130                135                140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145                150                155                160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
                165                170                175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
                180                185                190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
                195                200                205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210                215                220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225                230                235                240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```

				245					250				255			
Tyr	Val	Arg	Pro	Ser	Gln	Ser	His	Ser	Met	Gly	Phe	Asp	Lys	Val	Thr	
			260					265					270			
Ala	Val	Pro	Thr	Met	Val	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Thr	Tyr	Ser	
		275					280					285				
Leu	Arg	Asn	Glu	Lys	Val	Lys	Ala	Val	Leu	Lys	Glu	Ala	Val	Ser	Lys	
	290					295					300					
Ile	Met	Ser	Ser	Trp	His	Arg	Arg	Thr	Xaa	Asn	Phe					
305					310					315						

&lt;210&gt; 1129

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g45 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1129

Met	Glu	Pro	Gln	Asn	Thr	Thr	Gln	Val	Ser	Met	Phe	Val	Leu	Leu	Gly	
1				5					10					15		
Phe	Ser	Gln	Thr	Gln	Glu	Leu	Gln	Lys	Phe	Leu	Phe	Leu	Leu	Phe	Leu	
		20					25						30			
Leu	Val	Tyr	Val	Thr	Thr	Ile	Val	Gly	Asn	Leu	Leu	Ile	Met	Val	Thr	
	35					40						45				
Val	Thr	Phe	Asp	Cys	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Arg	
	50					55					60					
Asn	Leu	Ala	Leu	Ile	Asp	Leu	Cys	Tyr	Ser	Thr	Val	Thr	Ser	Pro	Lys	
65				70					75						80	
Met	Leu	Val	Asp	Phe	Leu	His	Glu	Thr	Lys	Thr	Ile	Ser	Tyr	Gln	Gly	
			85						90					95		
Cys	Met	Ala	Gln	Ile	Phe	Phe	Phe	His	Leu	Leu	Gly	Gly	Gly	Thr	Val	
		100						105					110			
Phe	Phe	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Ser	Gln	
	115						120					125				
Pro	Leu	Arg	Tyr	Val	Thr	Ile	Met	Asn	Thr	Gln	Leu	Cys	Val	Gly	Leu	
	130					135					140					
Val	Val	Ala	Ala	Trp	Val	Gly	Gly	Phe	Val	His	Ser	Ile	Val	Gln	Leu	
145				150					155					160		
Ala	Leu	Ile	Leu	Pro	Leu	Pro	Phe	Cys	Asp	Pro	Asn	Ile	Ile	Asp	Asn	
			165					170						175		
Phe	Tyr	Cys	Asp	Val	Pro	Gln	Val	Leu	Arg	Leu	Ala	Cys	Thr	Asp	Thr	
	180							185					190			
Ser	Leu	Leu	Glu	Phe	Leu	Met	Ile	Phe	Asn	Ser	Gly	Leu	Leu	Val	Ile	
	195					200						205				
Ile	Trp	Phe	Leu	Leu	Leu	Leu	Ile	Ser	Tyr	Thr	Val	Ile	Leu	Val	Met	
	210					215					220					
Leu	Arg	Ser	His	Ser	Gly	Lys	Ala	Arg	Arg	Lys	Ala	Ala	Ser	Thr	Cys	
225				230						235					240	
Thr	Thr	His	Ile	Ile	Val	Val	Ser	Met	Ile	Phe	Ile	Pro	Cys	Ile	Tyr	
			245						250					255		
Ile	Tyr	Thr	Trp	Pro	Phe	Thr	Pro	Phe	Leu	Met	Asp	Lys	Ala	Val	Ser	
	260							265					270			
Ile	Ser	Tyr	Thr	Val	Met	Thr	Pro	Met	Leu	Asn	Pro	Met	Ile	Tyr	Thr	
	275					280						285				
Leu	Arg	Asn	Gln	Asp	Met	Lys	Ala	Ala	Met	Arg	Arg	Leu	Gly	Lys	Cys	
	290					295					300					
Leu	Val	Ile	Cys	Arg	Glu											
305					310											

&lt;210&gt; 1130

<211> 311  
 <212> PRT  
 <213> Unknown (H38g46 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(311)  
 <223> Xaa = Any Amino Acid

<400> 1130  
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr  
 20 25 30  
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile  
 35 40 45  
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Phe Leu Ser His  
 50 55 60  
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu  
 65 70 75 80  
 Leu Glu Asn Leu Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys  
 85 90 95  
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe  
 100 105 110  
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val  
 130 135 140  
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa  
 145 150 155 160  
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe  
 165 170 175  
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys  
 180 185 190  
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser  
 195 200 205  
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro  
 210 215 220  
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu  
 225 230 235 240  
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val  
 245 250 255  
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe  
 260 265 270  
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg  
 275 280 285  
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu  
 290 295 300  
 Leu Cys Leu Ile Leu Xaa Asn  
 305 310

<210> 1131  
 <211> 334  
 <212> PRT  
 <213> Unknown (H38g47 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
          65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
          145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
          165          170          175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Ile Asn Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
          225          230          235          240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
          275          280          285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
          290          295          300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
          305          310          315          320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
          325          330

```

&lt;210&gt; 1132

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g48 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1132

```

Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
 1          5          10          15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
          20          25          30

```

Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Ile Ile Thr  
 35 40 45  
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
 50 55 60  
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly  
 85 90 95  
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val  
 100 105 110  
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg  
 115 120 125  
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu  
 130 135 140  
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu  
 145 150 155 160  
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn  
 165 170 175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val  
 195 200 205  
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met  
 210 215 220  
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr  
 245 250 255  
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser  
 260 265 270  
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His  
 290 295 300  
 Arg Leu Val  
 305

&lt;210&gt; 1133

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g49 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys  
 50 55 60  
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val  
 65 70 75 80  
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

```
<210> 1135
<211> 356
<212> PRT
<213> Unknown (H38g51 protein)
```



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10          15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20          25          30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35          40          45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
          50          55          60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65          70          75          80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85          90          95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100         105         110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115         120         125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
          130         135         140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
145         150         155         160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165         170         175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180         185         190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195         200         205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
210         215         220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225         230         235         240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245         250         255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260         265         270
Gly Lys Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275         280         285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
          290         295         300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
305         310         315         320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325         330         335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
          340         345         350
Arg Xaa Tyr Pro
          355

```

&lt;210&gt; 1136

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g52 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
 1           5           10           15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe
          20           25           30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
          35           40           45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65           70           75           80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
          100          105          110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
          115          120          125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
130          135          140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
145          150          155          160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
          165          170          175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
          180          185          190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Phe Ile
          195          200          205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225          230          235          240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
          245          250          255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
          260          265          270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
          275          280          285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
290          295          300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
305          310          315

```

&lt;210&gt; 1137

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g53 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
          35           40           45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
          50           55           60

```

```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65          70          75          80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
          85          90          95
Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
          100          105          110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
          115          120          125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
          130          135          140
Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser
145          150          155          160
Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
          165          170          175
Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
          180          185          190
Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
          195          200          205
Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
          210          215          220
Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser
225          230          235          240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
          245          250          255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe
          260          265          270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr
          275          280          285
Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly
          290          295          300
Lys Glu Met Gly Leu Thr Gln Ser
305          310

```

&lt;210&gt; 1138

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g54 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(343)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1138

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20          25          30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
          35          40          45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
          50          55          60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
          85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
          100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```

```

      115              120              125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
      130              135              140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
      145              150              155              160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165              170              175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180              185              190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195              200              205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210              215              220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
      225              230              235              240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245              250              255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260              265              270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275              280              285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290              295              300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
      305              310              315              320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325              330              335
Tyr Leu Ser Tyr Thr His His
      340

```

&lt;210&gt; 1139

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g55 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1              5              10              15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg His Thr
      20              25              30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35              40              45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50              55              60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
      65              70              75              80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85              90              95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100              105              110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115              120              125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130              135              140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
      145              150              155              160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165              170              175

```

Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala  
 180 185 190  
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly  
 195 200 205  
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val  
 210 215 220  
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln  
 225 230 235 240  
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val  
 245 250 255  
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys  
 260 265 270  
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln  
 275 280 285  
 Ala Gly Gln  
 290

&lt;210&gt; 1140

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g56 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile  
 1 5 10 15  
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile  
 20 25 30  
 Thr Gly Asn Gly Ala Ile Ala Phe Ala Leu Trp Cys Asp Arg Arg Leu  
 35 40 45  
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile  
 50 55 60  
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser  
 65 70 75 80  
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe  
 85 90 95  
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala  
 100 105 110  
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile  
 115 120 125  
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys  
 130 135 140  
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro  
 145 150 155 160  
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro  
 165 170 175  
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys  
 180 185 190  
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile  
 195 200 205  
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser  
 210 215 220  
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 225 230 235 240  
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

```

                245                250                255
Leu Gly His Ser Thr Glu Met Gln Lys Ile Val Thr Leu Phe Tyr Ala
                260                265                270
Met Val Thr Ser Leu Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys
                275                280                285
Glu Ile Lys Ala Ala Leu Arg Lys Val Leu Val Ser Ser Asn Ile Ile
                290                295                300
Xaa Gly Ile
305

```

&lt;210&gt; 1141

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g57 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(221)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1141

```

Ala Cys Lys His Asp Met Ile Leu Thr Val Met Ala Tyr Asp Cys Leu
 1                5                10                15
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His
                20                25                30
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Ile Ser Met Xaa Asp
                35                40                45
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn
 50                55                60
Val Glu Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu
 65                70                75                80
Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser
                85                90                95
Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Phe
                100                105                110
Lys Ile Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr
                115                120                125
Lys Ala Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe
                130                135                140
Tyr Gly Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Leu Ser Pro Pro
 145                150                155                160
Pro Arg Asn Gly Val Met Ala Ser Val Met Tyr Ala Val Val Thr Pro
                165                170                175
Met Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser
                180                185                190
Ala Leu Trp Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe
                195                200                205
His Pro Phe Ser Cys Val Gly Lys Gly Asn His Ile Lys
                210                215                220

```

&lt;210&gt; 1142

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g58 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1142

```

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1           5           10           15
Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
          20           25           30
Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
          35           40           45
Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
65           70           75           80
Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
          85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
          115          120          125
Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
          130          135          140
Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
145          150          155          160
Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
          165          170          175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
          195          200          205
Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
          210          215          220
Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
225          230          235          240
Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
          245          250          255
Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
          260          265          270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
          290          295          300
Ala Arg Arg Leu Gln Val Ser Leu Ser Met
305          310

```

&lt;210&gt; 1143

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g59 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1143

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1           5           10           15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20           25           30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
          35           40           45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

50		55		60	
Phe Phe Leu Ser Thr	Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser				
65	70	75	80		
Trp Glu Leu Xaa Val	Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile				
	85	90	95		
Ser Tyr Asn Ser Cys	Ser Val Gln Met Ile Thr His Leu Phe Leu Gly				
	100	105	110		
Thr Ala Gln Cys Leu	Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val				
	115	120	125		
Glu Ile Ser Tyr Leu	Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val				
	130	135	140		
Cys Ile Gln Leu Ala	Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala				
145	150	155	160		
Val Thr Leu Ile Ile	Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val				
	165	170	175		
Ile Asn His Phe Thr	Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys				
	180	185	190		
Ser Asp Thr Leu Val	Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe				
	195	200	205		
Thr Leu Pro Leu Pro	Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile				
210	215	220			
Phe Val Arg Ala Val	Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly				
225	230	235	240		
Ser His Leu Thr Gly	Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met				
	245	250	255		
Tyr Leu Lys Pro Gln	Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val				
	260	265	270		
Ser Lys Leu Tyr Gly	Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr				
	275	280	285		
Ile Gln Arg Asn Lys	Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys				
	290	295	300		
Gly Asn Glu Lys Ser	Xaa Gln Phe Ser Leu Asn				
305	310	315			

&lt;210&gt; 1144

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g61 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(351)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1144

Met Asp Ile Leu Val	Ile Asp Asn Gly Ser Glu Val Thr Glu Phe Ile
1	5 10 15
Leu Val Gly Leu Tyr	Asn His Pro Lys Phe Gln Ile Ala Phe Tyr Arg
	20 25 30
Thr Met Val Val Val	Tyr Leu Ile Thr Phe Val Gly Ser Ser Leu Ile
	35 40 45
Ile Val Val Val Lys	Val Asp Gly Trp Leu His Thr Pro Met Cys Phe
	50 55 60
Phe Leu Ser Asn Leu	Ser Phe Leu Asp Ile Cys Tyr Ser Ser Asn Ser
65	70 75 80
Val Pro Phe Leu Leu	Phe Asn Gly Leu Arg Asp Tyr Pro Thr Ile Ser
	85 90 95
Tyr Asn Ser Cys Tyr	Ala Gln Met Thr Ser Ala Phe Phe Leu Gly Met
	100 105 110



Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val  
 115 120 125  
 Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys  
 130 135 140  
 Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile  
 145 150 155 160  
 Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met  
 165 170 175  
 Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn  
 180 185 190  
 His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp  
 195 200 205  
 Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu  
 210 215 220  
 Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala  
 225 230 235 240  
 Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala  
 245 250 255  
 Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile  
 260 265 270  
 Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg  
 275 280 285  
 Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val  
 290 295 300  
 Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val  
 305 310 315 320  
 Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala  
 325 330 335  
 Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys  
 340 345 350

&lt;210&gt; 1145

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g62 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1145

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Gly Tyr Pro Lys Leu Glu Ile Ile Phe Phe Ala Leu Ile Leu  
 20 25 30  
 Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala  
 35 40 45  
 Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser  
 65 70 75 80  
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu  
 130 135 140  
 Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr  
 145 150 155 160  
 Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

                165                170                175
Phe Leu Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ser Asp Ile
                180                185                190
Ser Val Asn Ile Val Thr Leu Ala Val Ser Asn Ile Ala Phe Leu Val
                195                200                205
Leu Pro Leu Leu Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
                210                215                220
Ile Leu Arg Thr Asn Ser Ala Thr Gly Arg His Lys Ala Phe Ser Thr
225                230                235                240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
                245                250                255
Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Leu Gly Lys Asp Asn
                260                265                270
Leu Gln Ala Thr Glu Gly Leu Val Ser Met Phe Tyr Gly Val Val Thr
                275                280                285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
290                295                300
Ala Ala Ile Lys Tyr Leu Leu Ser Arg Lys Ala Ile Asn Gln
305                310                315

```

&lt;210&gt; 1146

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g63 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1146

```

Met Phe Pro Ala Asn Trp Thr Ser Val Lys Val Phe Phe Phe Leu Gly
1                5                10                15
Phe Phe His Tyr Pro Lys Val Gln Val Ile Ile Phe Ala Val Cys Leu
                20                25                30
Leu Met Tyr Leu Ile Thr Leu Leu Gly Asn Ile Phe Leu Ile Ser Ile
                35                40                45
Thr Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
50                55                60
Asn Leu Ser Phe Leu Asp Ile Trp Tyr Ser Ser Ser Ala Leu Ser Pro
65                70                75                80
Met Leu Ala Asn Phe Val Ser Gly Arg Asn Thr Ile Ser Phe Ser Gly
                85                90                95
Cys Ala Thr Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
                100                105                110
Val Leu Leu Pro Met Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
                115                120                125
Pro Leu Arg Tyr Pro Val Ile Met Asn Arg Arg Thr Cys Val Gln Ile
130                135                140
Ala Ala Gly Ser Trp Met Thr Gly Cys Leu Thr Ala Met Val Glu Met
145                150                155                160
Met Ser Val Leu Pro Leu Ser Leu Cys Gly Asn Ser Ile Ile Asn His
                165                170                175
Phe Thr Cys Glu Ile Leu Ala Ile Leu Lys Leu Val Cys Val Asp Thr
                180                185                190
Ser Leu Val Gln Leu Ile Met Leu Val Ile Ser Val Leu Leu Leu Pro
195                200                205
Met Pro Met Leu Leu Ile Cys Ile Ser Tyr Ala Phe Ile Leu Ala Ser
210                215                220
Ile Leu Arg Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Ser Thr
225                230                235                240
Cys Thr Ala His Leu Met Val Val Val Leu Phe Tyr Gly Thr Ala Leu
                245                250                255

```

Ser Met His Leu Lys Pro Ser Ala Val Asp Ser Gln Glu Ile Asp Lys  
                   260                  265                  270  
 Phe Met Ala Leu Val Tyr Ala Gly Gln Thr Pro Met Leu Asn Pro Ile  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Val Ala Leu Lys Lys Leu  
                   290                  295                  300  
 Leu Ile Arg Asn His Phe Asn Thr Ala Phe Ile Ser Ile Leu Lys  
 305                  310                  315

&lt;210&gt; 1147

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g64 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1147

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala  
 1                  5                  10                  15  
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu  
                   20                  25                  30  
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu  
                   35                  40                  45  
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser  
                   50                  55                  60  
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln  
 65                  70                  75                  80  
 Met Leu Ala Val Leu Leu Glu His Gly Ala Leu Ser Tyr Thr Arg  
                   85                  90                  95  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys  
                   100                  105                  110  
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln  
                   115                  120                  125  
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu  
                   130                  135                  140  
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr  
 145                  150                  155                  160  
 Val Ser Ala Phe Thr Leu Ser Phe Cys Gly Thr Ser Glu Ile Asp Phe  
                   165                  170                  175  
 Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Thr Cys Gly Glu Ser  
                   180                  185                  190  
 Tyr Thr Gln Glu Val Leu Ile Ile Met Phe Ala Ile Phe Val Ile Pro  
                   195                  200                  205  
 Ala Ser Met Val Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala  
                   210                  215                  220  
 Ile Met Gly Ile Pro Ala Gly Ser Gln Ala Lys Thr Phe Ser Thr Cys  
 225                  230                  235                  240  
 Thr Ser His Leu Thr Ala Val Ser Leu Phe Phe Gly Thr Leu Ile Phe  
                   245                  250                  255  
 Met Tyr Leu Arg Gly Asn Ser Asp Gln Ser Ser Glu Lys Asn Arg Val  
                   260                  265                  270  
 Val Ser Val Leu Tyr Thr Glu Val Ile Pro Met Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile Leu  
                   290                  295                  300  
 Asn Arg Ala Lys Leu Ser  
 305                  310

&lt;210&gt; 1148

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g65 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1           5           10           15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
          20           25           30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
          35           40           45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
          50           55           60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
65           70           75           80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
          85           90           95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
          100          105          110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
          115          120          125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
          130          135          140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145          150          155          160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
          165          170          175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
          180          185          190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
          195          200          205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
          210          215          220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225          230          235          240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
          245          250          255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
          260          265          270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Leu Arg Lys
          290          295          300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305          310          315          320
Ile

```

&lt;210&gt; 1149

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g66 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser  
                   20                  25                  30  
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile  
           35                  40                  45  
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser  
       50                  55                  60  
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys  
   65                  70                  75                  80  
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly  
                   85                  90                  95  
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met  
                   100                  105                  110  
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
       115                  120                  125  
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe  
       130                  135                  140  
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu  
   145                  150                  155                  160  
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser  
                   165                  170                  175  
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr  
       180                  185                  190  
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu  
       195                  200                  205  
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly  
       210                  215                  220  
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu  
   225                  230                  235                  240  
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr  
                   245                  250                  255  
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser  
                   260                  265                  270  
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser  
                   275                  280                  285  
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg  
       290                  295                  300  
 His Val Asn Ser Trp Lys Asn  
   305                  310

&lt;210&gt; 1150

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g67 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly  
   1                  5                  10                  15  
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu  
           20                  25                  30  
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu  
       35                  40                  45  
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser  
       50                  55                  60  
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln  
   65                  70                  75                  80  
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly  
                   85                  90                  95  
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

```

      100              105              110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115              120              125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
      130              135              140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
145              150              155
Val Leu Ile Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
      165              170              175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
      180              185              190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
      195              200              205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
      210              215              220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
225              230              235
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245              250              255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
      260              265              270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
      290              295              300
Leu Trp Lys Asn Tyr Asp Ser Arg
305              310

```

&lt;210&gt; 1151

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g68 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1151

```

Met Cys Ser Gly Asn Gln Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp
 1              5              10              15
Phe Thr Leu Thr Gly Leu Phe Ala Glu Ser Lys His Ala Ala Leu Leu
      20              25              30
Tyr Thr Val Thr Phe Leu Leu Phe Leu Met Ala Leu Thr Gly Asn Ala
      35              40              45
Leu Leu Ile Leu Leu Ile His Ser Glu Pro Arg Leu His Thr Pro Met
      50              55              60
Tyr Phe Phe Ile Ser Gln Leu Ala Leu Met Asp Leu Met Tyr Leu Cys
      65              70              75              80
Val Thr Val Pro Lys Met Leu Val Gly Gln Val Thr Gly Asp Asp Thr
      85              90              95
Ile Ser Pro Ser Gly Cys Gly Ile Gln Met Phe Phe His Leu Thr Leu
      100              105              110
Ala Gly Ala Glu Val Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115              120              125
Ala Ala Val Cys Arg Pro Leu His Tyr Pro Leu Leu Met Asn Gln Arg
      130              135              140
Val Cys Gln Leu Leu Val Ser Ala Cys Trp Val Leu Gly Met Val Asp
      145              150              155              160
Gly Leu Leu Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Gln Ser
      165              170              175
Arg Lys Ile Leu Ser Phe Phe Cys Glu Thr Pro Ala Leu Leu Lys Leu
      180              185              190

```

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys  
 195 200 205  
 Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr  
 210 215 220  
 Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg  
 225 230 235 240  
 Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu  
 245 250 255  
 Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr  
 260 265 270  
 Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro  
 275 280 285  
 Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg  
 290 295 300  
 Ala Met Arg Ser Met Met Gln Ser Arg  
 305 310

&lt;210&gt; 1152

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g69 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1152

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser  
 20 25 30  
 Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr  
 35 40 45  
 Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr  
 50 55 60  
 Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys  
 65 70 75 80  
 Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile  
 100 105 110  
 Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu  
 130 135 140  
 Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val  
 145 150 155 160  
 Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr )  
 180 185 190  
 Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu  
 195 200 205  
 Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr  
 210 215 220  
 Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Thr Ala His Phe Ile Val Val Phe Leu Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

```
<210> 1153
<211> 310
<212> PRT
<213> Unknown (H38g70 protein)
```

[illegible]

```
<210> 1154
<211> 323
<212> PRT
<213> Unknown (H38g71 protein)
```



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
          50           55           60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
65          70           75           80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
          85           90           95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
          100          105          110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
          115          120          125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
          130          135          140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145          150          155          160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
          165          170          175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
          180          185          190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
          195          200          205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
          210          215          220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
225          230          235          240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
          245          250          255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
          260          265          270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
          275          280          285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
          290          295          300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
305          310          315          320
Phe Leu Cys

```

&lt;210&gt; 1155

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g72 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1155

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

```

1           5           10           15
Leu Ser Ser Ser Leu Glu Leu Gln Ile Phe Tyr Phe Leu Phe Phe Ser
      20      25      30
Ile Val Tyr Ala Ala Thr Val Leu Gly Asn Leu Leu Ile Val Val Thr
      35      40      45
Ile Ala Ser Glu Pro His Leu His Ser Pro Thr Tyr Phe Leu Leu Gly
      50      55      60
Asn Leu Ser Phe Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
      65      70      75      80
Met Ile Ala Asp Phe Leu Arg Glu His Lys Ala Ile Ser Phe Glu Gly
      85      90      95
Cys Met Thr Gln Met Phe Phe Leu His Leu Leu Gly Gly Ala Glu Ile
      100      105      110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Leu Thr Ile Met Ser Arg Arg Met Cys Val Gly Leu
      130      135      140
Val Ile Leu Ser Trp Ile Val Gly Ile Phe His Ala Leu Ser Gln Leu
      145      150      155      160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
      165      170      175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Val Asp Thr
      180      185      190
Tyr Ile Leu Gly Val Phe Met Ile Ser Thr Ser Gly Met Ile Ala Leu
      195      200      205
Val Cys Phe Ile Leu Leu Val Ile Ser Tyr Thr Ile Ile Leu Val Thr
      210      215      220
Val Arg Gln Arg Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Cys
      225      230      235      240
Ser Ala His Phe Thr Val Val Thr Leu Phe Phe Gly Pro Cys Thr Phe
      245      250      255
Ile Tyr Val Trp Pro Phe Thr Asn Phe Pro Ile Asp Lys Val Leu Ser
      260      265      270
Val Phe Tyr Thr Ile Tyr Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275      280      285
Val Arg Asn Lys Asp Val Lys Tyr Ser Met Arg Lys Leu Ser Ser His
      290      295      300
Ile Phe Lys Ser Arg Lys Thr Asp His Thr Pro
      305      310      315

```

&lt;210&gt; 1156

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g73 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1156

```

Met Lys Lys Tyr Met Glu Arg Thr Asn Xaa Thr Thr Glu Phe Glu Leu
1           5           10           15
Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu Phe
      20      25      30
Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg Ile
      35      40      45
Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His Gly
      50      55      60

```

```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65          70          75          80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85          90          95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115        120        125
Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys Lys
      130        135        140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145          150        155        160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165        170        175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180        185        190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195        200        205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
210          215          220
Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225          230        235        240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245        250        255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260        265        270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275        280        285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
290          295        300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305          310        315        320
Trp

```

&lt;210&gt; 1157

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g74 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1157

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20          25          30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35          40          45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50          55          60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65          70          75          80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85          90          95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```

```

      100      105      110
Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe
      115      120      125
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His
      130      135      140
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp
145      150      155      160
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn
      165      170      175
Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu
      180      185      190
Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser
      195      200      205
Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys
      210      215      220
Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys
225      230      235      240
Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp
      245      250      255
Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro
      260      265      270
Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
      275      280      285
Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala
      290      295      300
Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro
305      310      315      320
Ser Phe Phe Leu Cys
      325

```

&lt;210&gt; 1158

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g75 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1158

```

Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe
 1      5      10      15
Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Val Leu Leu Pro
      20      25      30
Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val
      35      40      45
Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn
      50      55      60
Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val
65      70      75      80
Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu
      100      105      110
Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro
      115      120      125
Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val
      130      135      140
Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile
145      150      155      160
Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe
      165      170      175

```

Phe Cys Asp Ser Gly Pro Leu Leu Ala Leu Ala Cys Ala Asp Thr Thr  
 180 185 190  
 Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys  
 195 200 205  
 Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile  
 210 215 220  
 Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe  
 245 250 255  
 Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile  
 260 265 270  
 Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp  
 290 295 300  
 Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu  
 305 310 315

&lt;210&gt; 1159

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g76 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1159

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
 35 40 45  
 Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met  
 100 105 110  
 Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu  
 130 135 140  
 Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val  
 145 150 155 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
 180 185 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
 195 200 205  
 Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
 210 215 220  
 Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser  
 225 230 235 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
 245 250 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

			260					265					270				
Val	Ser	Val	Phe	His	Thr	Val	Ile	Phe	Pro	Leu	Leu	Asn	Pro	Ile	Ile		
		275					280					285					
Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Ala	Ala	Met	Arg	Lys	Val	Val		
	290					295					300						
Thr	Lys	Tyr	Ile	Leu	Cys	Glu	Glu	Lys									
305					310												

&lt;210&gt; 1160

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g77 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1160

Met	Glu	Ser	Gln	Arg	Asn	Ile	Xaa	Lys	Phe	Ile	Leu	Met	Ser	Leu	Ser		
1				5					10					15			
Ser	Ile	Gln	Asn	Ile	Gln	Ile	Phe	Val	Phe	Val	Phe	Leu	Phe	Cys	Asn		
		20					25					30					
Val	Ala	Ile	Leu	Val	Gly	Asn	Phe	Leu	Ile	Leu	Ile	Ser	Ile	Xaa	Cys		
	35					40					45						
Ser	Pro	Leu	Phe	Asn	Gln	Pro	Met	His	Tyr	Phe	Leu	Gly	Tyr	Met	Asn		
	50				55						60						
Ile	Tyr	Tyr	Thr	Ser	Cys	Val	Thr	Pro	Lys	Ile	Ile	Gly	Asp	Leu	Val		
65				70					75					80			
Val	Gly	Arg	Ile	Asn	Ile	Ser	Tyr	Asp	Arg	Ile	Phe	Pro	Met	His	Phe		
			85					90						95			
Phe	Gly	Ile	Ile	Glu	Ile	Phe	Ile	Leu	Thr	Val	Met	Ala	Phe	Asp	His		
	100						105					110					
Tyr	Val	Ala	Ile	Cys	Lys	Pro	Pro	Arg	Tyr	Leu	Ile	Ile	Met	Asn	Arg		
	115					120					125						
Thr	Lys	Tyr	Asn	Thr	Leu	Ile	Ser	Val	Ala	Trp	Leu	Leu	Gly	Leu	Ile		
	130				135					140							
His	Ser	Leu	Phe	Gln	Phe	Ser	Met	Lys	Ile	Trp	Leu	Pro	Phe	Cys	Gly		
145				150					155						160		
Ser	Asn	Lys	Val	Asp	Xaa	Tyr	Xaa	Asp	Ile	Phe	Pro	Leu	Leu	Lys			
			165					170					175				
Val	Ala	Cys	Thr	Asp	Thr	Cys	Ile	Thr	Gly	Val	Leu	Val	Val	Ala	Asn		
	180						185					190					
Ser	Gly	Met	Phe	Ala	Leu	Val	Thr	Phe	Val	Leu	Ser	Phe	Gly	Ser	Tyr		
	195					200					205						
Val	Ile	Ile	Leu	Phe	Pro	Leu	Lys	Asn	His	Ser	Val	Glu	Gly	Arg	Cys		
	210					215					220						
Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Ile	Thr	Met	Val	Ile	Phe	Phe		
225				230					235					240			
Phe	Glu	Pro	Ser	Ile	Phe	Ala	Tyr	Leu	Arg	Pro	Ser	Thr	Phe	Pro	Glu		
			245						250					255			
Asp	Lys	Ile	Ser	Ala	Leu	Phe	Tyr	Thr	Ile	Ile	Ala	Pro	Met	Phe	Asn		
	260						265					270					
His	Leu	Ile	Tyr	Asn	Leu	Arg	Asn	Thr	Glu	Met	Lys	Lys	Ala	Met	Arg		
	275					280						285					
Lys	Val	Trp	Tyr	Gln	Ile	Ser	Phe	Ser	Glu	Glu	Lys	Gln	Leu	Ile	Cys		
	290				295						300						
Pro	Thr	Xaa	Cys	Thr	Lys	Glu	Leu	Tyr									
305					310												

<210> 1161  
 <211> 304  
 <212> PRT  
 <213> Unknown (H38g78 protein)

<220>  
 <223> Synthetic construct

<400> 1161

```

Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1           5           10           15
Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
          20           25           30
Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
          35           40           45
Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
          50           55           60
Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
          65           70           75           80
Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
          85           90           95
Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
          100          105          110
Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
          115          120          125
His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
          130          135          140
Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
          145          150          155          160
Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
          165          170          175
Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
          180          185          190
Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
          195          200          205
Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
          210          215          220
Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
          225          230          235          240
Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
          245          250          255
Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
          260          265          270
Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
          275          280          285
Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
          290          295          300

```

<210> 1162  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g79 protein)

<220>  
 <223> Synthetic construct

<400> 1162

```

Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1           5           10           15
Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

```

```
<210> 1163
<211> 323
<212> PRT
<213> Unknown (H38g80 protein)
```

```
<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid
```

504



Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pro Lys Val Leu  
 65 70 75 80  
 Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe  
 85 90 95  
 Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu  
 100 105 110  
 Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu  
 115 120 125  
 His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu  
 130 135 140  
 Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu  
 145 150 155 160  
 Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe  
 165 170 175  
 Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu  
 180 185 190  
 Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr  
 195 200 205  
 Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu  
 210 215 220  
 His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser  
 225 230 235 240  
 Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met  
 245 250 255  
 Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val  
 260 265 270  
 Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val  
 290 295 300  
 Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser  
 305 310 315 320  
 Ile Pro Arg

&lt;210&gt; 1164

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g81 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1164

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu  
 1 5 10 15  
 Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile  
 20 25 30  
 Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe  
 35 40 45  
 Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu  
 50 55 60  
 Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro  
 65 70 75 80  
 Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg  
 85 90 95  
 Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu  
 100 105 110  
 Gly Leu Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

130	135	140
Met Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln		
145	150	155
Val Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp		160
	165	170
Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp		175
	180	185
Thr Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr		190
	195	200
Leu Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys		205
	210	215
His Val Arg Lys Ala Ala Ser Glu Leu Lys Asn Lys Ala Met Ser Thr		220
225	230	235
Cys Thr Thr His Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile		240
	245	250
Phe Ile Tyr Met His Pro Phe Arg Ala Leu Pro Ala Asp Lys Val Val		255
	260	265
Ser Phe Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr		270
	275	280
Thr Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser		285
	290	295
Arg His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn		300
305	310	315

&lt;210&gt; 1165

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g82 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1165

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu		
1	5	10
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu		15
	20	25
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr		30
	35	40
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys		45
	50	55
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe		60
65	70	75
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys		80
	85	90
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys		95
	100	105
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe		110
	115	120
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys		125
	130	135
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln		140
145	150	155
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa		160
	165	170
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr		175
	180	185
		190

Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys  
 195 200 205  
 Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile  
 210 215 220  
 Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr  
 225 230 235 240  
 Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr  
 245 250 255  
 Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu  
 260 265 270  
 Gly Ser Thr Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr  
 275 280 285

&lt;210&gt; 1166

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g83 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1166

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Gln Ser Gln Asp Ile Gln Leu Val Phe Val Leu Val Leu  
 20 25 30  
 Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr  
 35 40 45  
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Thr Val Ala Pro Arg  
 65 70 75 80  
 Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly  
 85 90 95  
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly  
 100 105 110  
 Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met  
 130 135 140  
 Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val  
 145 150 155 160  
 Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn  
 165 170 175  
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu  
 195 200 205  
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg  
 210 215 220  
 Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys  
 225 230 235 240  
 Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe  
 245 250 255  
 Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser  
 260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys  
 290 295 300  
 His Ile Ala

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Leu Gly  
 50 55 60  
 Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu  
 85 90 95  
 Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu  
 130 135 140  
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu  
 145 150 155 160  
 Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His  
 165 170 175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser  
 180 185 190  
 Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val  
 195 200 205  
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr  
 210 215 220  
 Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr  
 225 230 235 240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr  
 245 250 255  
 Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
 260 265 270  
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met  
 290 295 300  
 Phe Lys Ser Asn Val  
 305

&lt;210&gt; 1207

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g124 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1207

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr  
 20 25 30  
 Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala  
 35 40 45  
 Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser  
 50 55 60  
 Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr  
 65 70 75 80  
 Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr  
 85 90 95  
 Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu Leu

305

&lt;210&gt; 1167

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g84 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
 20          25          30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
 35          40          45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
 50          55          60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
 65          70          75          80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
 85          90          95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
 100          105          110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115          120          125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
 130          135          140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
 145          150          155          160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
 165          170          175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
 180          185          190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
 195          200          205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
 210          215          220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225          230          235          240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245          250          255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
 260          265          270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275          280          285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
 290          295          300
Ala Leu Ala Gly Lys

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305

&lt;210&gt; 1168

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g85 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1          5          10          15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
 20          25          30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
 35          40          45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
 50          55          60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
 65          70          75          80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
 85          90          95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
 100          105          110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
 115          120          125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
 130          135          140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
 145          150          155          160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
 165          170          175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
 180          185          190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Leu Ile Ser Tyr Thr
 195          200          205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
 210          215          220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
 225          230          235          240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
 245          250          255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
 260          265          270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
 275          280          285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
 290          295          300
Leu Ile Gly Leu Asp Leu Leu
305          310

```

&lt;210&gt; 1169

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g86 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1          5          10          15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

		20					25				30			
Gly	His	Ser	Val	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Ile	His	Gly	Glu
		35					40				45			
Leu	Val	Phe	Ser	Leu	Phe	Ser	Phe	Val	Phe	Val	Phe	Gln	Met	Tyr
		50				55					60			
Ser	Phe	Val	Ile	Leu	Ile	Lys	Met	Ile	Met	Asn	Ser	Ile	Ser	Arg
65					70					75				80
Tyr	Ile	Thr	Thr	Asn	Leu	Lys	Cys	Lys	Thr	Ser	Ala	Leu	Val	Phe
				85					90					95
Cys	Phe	Ala	Ile	Ser	Glu	Thr	Leu	Ile	Leu	Leu	Ala	Trp	Gly	Cys
			100					105					110	
Gly	Ile	Cys	Val	Pro	Gln	Val	Cys	Ser	Leu	Thr	Met	Leu	Gly	His
		115					120					125		
Gly	Val	Gly	Ile	Asp	Gly	Val	Met	Ala	His	Pro	Glu	Ala	Met	Val
130					135						140			
Leu	Ser	Phe	Cys	Asp	Arg	Ser	Ile	Ile	Asn	His	Cys	Val	Trp	Thr
145					150					155				160
Ser	Phe	His	Gln	Thr	Leu	Leu	Arg	Ala	Pro	Ala	Ser	Gln	Ala	Gly
			165						170					175
Phe	Val	Val	Ile	Ala	Xaa	Xaa	Leu	Ile	Ile	Phe	Ile	Ser	Asp	Ile
			180					185					190	
Ile	Leu	Ser	Thr	Ile	Leu	His	Phe	Leu	Phe	Pro	Glu	Ala	Asn	Ser
		195					200					205		Lys
Ala	Phe													
	210													

&lt;210&gt; 1170

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g87 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1170

Met	Gly	Asn	Leu	Gly	Met	Ile	Met	Val	Ile	Arg	Ile	Asn	Pro	Lys	Leu
1				5					10					15	
His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His	Leu	Ser	Phe	Val	Asp	Phe
			20					25					30		
Cys	Tyr	Ser	Thr	Thr	Ile	Thr	Pro	Lys	Leu	Leu	Glu	Asn	Leu	Val	Val
		35					40					45			
Glu	Asp	Arg	Ile	Ile	Ser	Phe	Thr	Gly	Cys	Ile	Met	Gln	Phe	Phe	Phe
	50					55				60					
Ala	Cys	Ile	Phe	Val	Val	Thr	Glu	Thr	Phe	Met	Leu	Ala	Ala	Met	Ala
65					70					75					80
Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	Asn	Pro	Leu	Leu	Tyr	Thr	Val	Ala
			85						90					95	
Met	Ser	Gln	Arg	Leu	Cys	Ser	Leu	Leu	Val	Ala	Ala	Ser	Tyr	Ser	Trp
			100					105					110		
Ser	Leu	Val	Cys	Ser	Leu	Thr	Tyr	Thr	Tyr	Phe	Leu	Leu	Thr	Leu	Ser
		115					120					125			
Phe	Cys	Arg	Thr	Asn	Phe	Ile	Asn	Asn	Phe	Val	Cys	Glu	His	Ala	Ala
	130					135						140			
Ile	Val	Ala	Val	Ser	Cys	Ser	Asp	Pro	Tyr	Met	Ser	Gln	Lys	Val	Ile
145					150					155					160
Leu	Val	Ser	Ala	Thr	Phe	Asn	Glu	Ile	Ser	Ser	Leu	Val	Ile	Ile	Leu
				165					170					175	
Thr	Ser	Tyr	Ala	Phe	Ile	Phe	Ile	Thr	Val	Met	Lys	Met	Pro	Ser	Thr
			180					185					190		
Gly	Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala
		195					200					205			

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn  
 210 215 220  
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr  
 225 230 235 240  
 Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys  
 245 250 255  
 Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys  
 260 265 270  
 His Lys

&lt;210&gt; 1171

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g88 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(348)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1171

Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser  
 1 5 10 15  
 His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser  
 20 25 30  
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser  
 35 40 45  
 Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu  
 50 55 60  
 Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu  
 65 70 75 80  
 Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val  
 85 90 95  
 Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly  
 130 135 140  
 Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val  
 145 150 155 160  
 Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe  
 165 170 175  
 Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp  
 180 185 190  
 Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Pro  
 195 200 205  
 Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile  
 210 215 220  
 Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val  
 245 250 255  
 Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile  
 260 265 270  
 Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg



290		295		300
Asp Leu Gly Thr Xaa Lys Met Lys Gln Ser Thr Gln Arg Ser Thr Phe				
305		310		315
Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys				
	325		330	335
Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu				
	340		345	

&lt;210&gt; 1172

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g89 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1172

Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly				
1	5		10	15
Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser				
	20		25	30
Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr				
	35		40	45
Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly				
	50		55	60
Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys				
	65		70	75
Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly				
	85		90	95
Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met				
	100		105	110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys				
	115		120	125
Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu				
	130		135	140
Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu				
	145		150	155
Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser				
	165		170	175
Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser				
	180		185	190
Tyr Ile Ile Glu Ile Leu Ile Val Val Asn Ser Gly Ile Leu Ser Leu				
	195		200	205
Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr				
	210		215	220
Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu				
	225		230	235
Ala Ser His Ile Ala Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe				
	245		250	255
Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala				
	260		265	270
Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr				
	275		280	285
Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His				
	290		295	300
Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg				
305	310		315	

&lt;210&gt; 1173

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
 1           5           10           15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
          20           25           30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
          35           40           45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
          50           55           60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
65           70           75           80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
          85           90           95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
          100          105          110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
          130          135          140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
145          150          155          160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
          165          170          175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
          180          185          190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
          195          200          205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
          210          215          220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
          245          250          255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
          260          265          270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
          290          295          300
Cys Arg Lys Leu Val Ser Xaa Lys
305          310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

```

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

```

1           5           10           15
Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
20           25           30
Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
35           40           45
Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
65           70           75           80
Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
85           90           95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
100          105          110
Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
115          120          125
Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
130          135          140
Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
145          150          155          160
Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
180          185          190
Thr Ala Asn Glu Ala Glu Leu Phe Ile Ser Val Leu Phe Leu Leu
195          200          205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
210          215          220
Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
260          265          270
Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
290          295          300
Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
305          310          315          320
Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
325          330          335
Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
340          345          350
Gln Arg Lys Phe Pro
355

```

&lt;210&gt; 1175

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g92 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1175

```

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
1           5           10           15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala  
 85 90 95  
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe  
 130 135 140  
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg  
 145 150 155 160  
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp  
 180 185 190  
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly  
 195 200 205  
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210 215 220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly  
 245 250 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly  
 260 265 270  
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
 290 295 300  
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315 320

&lt;210&gt; 1176

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g93 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser  
 20 25 30  
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
 35 40 45  
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys

```

65          70          75          80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85          90          95
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100         105         110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115         120         125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130         135         140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145         150         155         160
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165         170         175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180         185         190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195         200         205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210         215         220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
225         230         235         240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245         250         255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260         265         270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275         280         285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
      290         295         300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305         310

```

&lt;210&gt; 1177

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g94 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(338)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
 1          5          10          15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20          25          30
Gln Leu Glu His Ile Ile Ser Val Val Phe Ile Ile Tyr Ile Val
      35          40          45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
      50          55          60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
65          70          75          80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85          90          95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100         105         110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Ala Val
      115         120         125

```

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130          135          140
Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
145          150          155          160
Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
          165          170          175
His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
          180          185          190
Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
          195          200          205
Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
          210          215          220
Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
225          230          235          240
Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
          245          250          255
Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
          260          265          270
Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
          275          280          285
Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
          290          295          300
Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
305          310          315          320
Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
          325          330          335
Phe Ile

```

&lt;210&gt; 1178

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g95 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1178

```

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1          5          10          15
Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
          20          25          30
Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Val Pro Lys
65          70          75          80
Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
          85          90          95
Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
          100          105          110
Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Thr Val Val Leu Ser Pro Lys Asn Cys Ala Leu
          130          135          140
Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
          165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
          180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
          195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
          210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
          245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
          260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
          275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
          290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

&lt;210&gt; 1179

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g96 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
          20          25          30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
          35          40          45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
          85          90          95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
          130          135          140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
          180          185          190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
          195          200          205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
          210          215          220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225          230          235          240

```

Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile  
                           245                          250                          255  
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr  
                           260                          265                          270  
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe  
                           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser  
                           290                          295                          300  
 Leu Gln His Lys Glu Asn Phe Phe Val Phe  
 305                          310

&lt;210&gt; 1180

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g97 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1180

Met Ala Ala Glu Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Ala Gly  
 1                          5                          10                          15  
 Leu Ile His Gln Pro Gly Leu Gln Val Pro Val Phe Phe Leu Phe Leu  
                           20                          25                          30  
 Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu  
                           35                          40                          45  
 Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe  
                           50                          55                          60  
 Asn Leu Ser Leu Val Asp Phe Ser Phe Ser Thr Thr Ile Ile Pro Lys  
 65                          70                          75                          80  
 Met Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly  
                           85                          90                          95  
 Cys Met Ser Gln Phe Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser  
                           100                          105                          110  
 Phe Ile Leu Ser Ala Met Val Xaa Asp Arg Tyr Val Gly Ile Cys Asn  
                           115                          120                          125  
 Pro Leu Leu Tyr Thr Ile Thr Met Ser Pro Gln Val Cys Leu Leu Leu  
                           130                          135                          140  
 Leu Leu Gly Val Tyr Gly Met Gly Val Phe Gly Ala Val Ala His Thr  
 145                          150                          155                          160  
 Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His  
                           165                          170                          175  
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Gly Ser  
                           180                          185                          190  
 Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val Thr Val Gly Ile Gly  
                           195                          200                          205  
 Val Pro Ile Val Ala Val Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser  
                           210                          215                          220  
 Ile Leu Arg Val Ser Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Ser  
 225                          230                          235                          240  
 Cys Ser Ser Tyr Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala  
                           245                          250                          255  
 Phe Thr Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys  
                           260                          265                          270  
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Phe Asn Pro Leu  
                           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg Thr



290                      295                      300  
 Phe Ser Arg Ile Ser Phe Ser Glu Lys Asn Phe Arg Asn Arg Lys Glu  
 305                      310                      315                      320  
 Ile Leu Gly Phe Phe Xaa Asn Gln Ile Ala Phe  
                     325                      330

<210> 1181  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g98 protein)

<220>  
 <223> Synthetic construct

<400> 1181  
 Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu  
 1                      5                      10                      15  
 Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu  
                     20                      25                      30  
 Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu  
                     35                      40                      45  
 Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met  
                     50                      55                      60  
 Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser  
 65                      70                      75                      80  
 Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met  
                     85                      90                      95  
 Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly  
                     100                      105                      110  
 Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr  
                     115                      120                      125  
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser  
                     130                      135                      140  
 Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His  
 145                      150                      155                      160  
 Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser  
                     165                      170                      175  
 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile  
                     180                      185                      190  
 Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser  
                     195                      200                      205  
 Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr  
                     210                      215                      220  
 Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg  
 225                      230                      235                      240  
 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr  
                     245                      250                      255  
 Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala  
                     260                      265                      270  
 Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro  
                     275                      280                      285  
 Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp  
                     290                      295                      300  
 Ser Phe Thr Lys Met Val Lys Arg Asn Val  
 305                      310

<210> 1182  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g99 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
      20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
      35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
      65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
      85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
      100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
      130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
      145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
      165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
      180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
      195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
      210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
      225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
      245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
      260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
      290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
      305          310

```

&lt;210&gt; 1183

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g100 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

```

      20      25      30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
      50      55      60
Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
      65      70      75      80
Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Val Ser Leu Pro Glu
      85      90      95
Ser Lys Ile Gln Phe Phe Ser Phe Ala Ile Ser Val Thr Thr Glu Cys
      100      105      110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys Ile Arg Leu
      130      135      140
Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Gly Phe Leu Phe Arg
      145      150      155      160
Leu Thr Phe Cys Asn Ser Asn Val Val His His Ile Tyr Cys Asp Ile
      165      170      175
Ile Pro Leu Ser Lys Ile Ser Cys Thr Asp Ser Ser Ile Asn Phe Leu
      180      185      190
Met Val Phe Ile Phe Ser Gly Ser Ile Gln Val Phe Thr Ile Gly Thr
      195      200      205
Gly Leu Ile Ser Tyr Thr Phe Val Leu Phe Thr Ile Leu Lys Lys Lys
      210      215      220
Ser Val Lys Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ala His Leu
      225      230      235      240
Leu Ser Val Ser Leu Tyr His Gly Pro Leu Asp Phe Met Tyr Met Gly
      245      250      255
Ser Ala Ser Pro Gln Ala Asp Asp Glu Asp Met Met Glu Ser Leu Phe
      260      265      270
Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Thr Tyr Ser Leu Arg
      275      280      285
Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met Phe Lys Arg Asn Asn
      290      295      300
Ile Xaa Ile Ser Tyr Ser
      305      310

```

&lt;210&gt; 1184

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g101 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(231)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1184

```

Phe Cys Leu Phe Pro Ala Thr Val Ser Lys Ala Val Val Lys Phe Leu
  1           5           10           15
Ala Glu Thr Ile Ser Phe Ser Tyr Tyr Val Ile Gln Met Leu Val Phe
      20      25      30
Leu Phe Phe Val Thr Thr Glu Cys Asn Leu Leu Ala Ser Leu Gly Lys
      35      40      45
Asp Ile Tyr Met Pro Ile Arg Gln Pro Met Leu Tyr Pro Val Thr Met
      50      55      60
Ser Gln Val Cys Cys Ile Gln Leu Val Ala Ser Cys Tyr Gly His Gly
      65      70      75      80

```

```

Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe
      85                      90          95
Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu
      100                    105          110
Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe
      115                    120          125
Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val
      130                    135          140
Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val
      145                    150          155          160
Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile
      165                    170          175
Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser
      180                    185          190
Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val
      195                    200          205
Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln
      210                    215          220
Val Ile Cys Phe Leu Glu Asn
      225                    230

```

&lt;210&gt; 1185

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g102 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(216)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1185

```

Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val
  1      5      10      15
Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg
      20      25      30
Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe
      35      40      45
Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu
      50      55      60
Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala
      65      70      75      80
Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile
      85      90      95
Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser
      100     105     110
Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr
      115     120     125
Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn
      130     135     140
Asn Phe Ser Asp Leu Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val
      145     150     155     160
Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His
      165     170     175
Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys
      180     185     190
His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn
      195     200     205
Phe Leu Met Ala His Ile His Ile

```

210

215

<210> 1186  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g103 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(312)  
 <223> Xaa = Any Amino Acid

<400> 1186  
 Phe Met Glu Asn Arg Asn Ile Val Thr Val Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Gln Asn Lys Asn Ile Glu Val Phe Trp Phe Val Leu Phe Val Phe  
 20 25 30  
 Cys Tyr Ile Ala Ile Trp Met Glu Asn Phe Ile Ile Met Ile Ser Ile  
 35 40 45  
 Met Tyr Ile Xaa Leu Ile Asp Gln Pro Met Tyr Phe Phe Leu Asn Tyr  
 50 55 60  
 Leu Ala Leu Ser Asp Leu Cys Tyr Ile Ser Thr Val Ala Pro Lys Leu  
 65 70 75 80  
 Met Ile Asp Leu Leu Thr Glu Arg Lys Ile Val Ser Tyr Asn Asn Cys  
 85 90 95  
 Met Ile Gln Leu Phe Ile Thr His Phe Leu Gly Asp Ile Glu Ile Phe  
 100 105 110  
 Ile Leu Lys Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Lys His  
 115 120 125  
 Leu His Tyr Thr Ile Ile Thr Thr Lys Gln Ser Cys Asn Thr Ile Ile  
 130 135 140  
 Ile Ala Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu  
 145 150 155 160  
 Leu Thr Ile Phe Leu Pro Phe Cys Gly Leu Asn Glu Ile Asp Gln Tyr  
 165 170 175  
 Phe Cys Tyr Val Tyr Pro Leu Leu Lys Leu Ala Arg Ile Asp Ile Tyr  
 180 185 190  
 Arg Ile Gly Phe Leu Val Ile Val Asn Ser Gly Leu Ile Ser Leu Leu  
 195 200 205  
 Ala Phe Val Ile Leu Met Val Ser Tyr Tyr Leu Ile Leu Ser Thr Ile  
 210 215 220  
 Arg Val Tyr Ser Ala Glu Ser His Thr Lys Ala Leu Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Ile Ile Val Val Val Leu Phe Phe Val Pro Ala Leu Phe Ile  
 245 250 255  
 Tyr Ile Arg Pro Ala Ile Thr Phe Pro Glu Asp Lys Val Phe Val Leu  
 260 265 270  
 Phe Cys Ala Ile Ile Ala Pro Met Phe Ser Leu Leu Ile Tyr Met Leu  
 275 280 285  
 Arg Lys Val Glu Met Lys Asn Ala Val Arg Lys Met Trp Cys His Gln  
 290 295 300  
 Leu Leu Leu Ala Arg Lys Xaa Leu  
 305 310

<210> 1187  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g104 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1           5           10           15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
      20           25           30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
      35           40           45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65           70           75           80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
      85           90           95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
      100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
      115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
      130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
      165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
      180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
      195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
      210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
      245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
      260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
      290          295          300
Leu Lys Arg Thr
305

```

&lt;210&gt; 1188

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g105 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

                20                25                30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
   35                40                45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Phe Leu Ser
   50                55                60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
   65                70                75                80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
                85                90                95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
                100                105                110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
                115                120                125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
                130                135                140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
   145                150                155                160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
                165                170                175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
                180                185                190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Gly Val
                195                200                205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
                210                215                220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
   225                230                235                240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
                245                250                255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
                260                265                270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
                275                280                285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
                290                295                300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
   305                310                315                320
Lys Arg Met Leu

```

&lt;210&gt; 1189

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g106 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
  1                5                10                15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
                20                25                30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
                35                40                45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
                50                55                60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
   65                70                75                80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
                85                90                95

```

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
      100      105      110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
      115      120      125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
      130      135      140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145      150      155      160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
      165      170      175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
      180      185      190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
      195      200      205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
      210      215      220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
225      230      235      240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
      245      250      255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
      260      265      270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
      275      280      285
Leu Arg Asn
      290

```

&lt;210&gt; 1190

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g107 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1190

```

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Gly Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu
      85      90      95
Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp
      100      105      110
Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe
      130      135      140
Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His
145      150      155      160
Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser
      165      170      175
Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp
      180      185      190
Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly

```



```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
  210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
  305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

&lt;210&gt; 1191

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g108 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
  65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
  145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
  225              230              235              240

```

```
<210> 1192
<211> 295
<212> PRT
<213> Unknown (H38g109 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(295)
<223> Xaa = Any Amino Acid
```

<400>	1192																
Ile	Gln	Cys	Lys	Gly	Xaa	Xaa	Lys	Xaa	Ile	Lys	Thr	Phe	Ser	Val	Thr		
1				5					10					15			
Pro	Ile	Leu	Asn	Gly	Asn	Arg	Glu	Ile	Ala	Arg	Phe	Leu	Ser	Asn	Leu		
			20					25					30				
Ser	Leu	Ala	Gly	Ile	Gly	Phe	Pro	Ser	Thr	Ile	Val	Ser	Lys	Met	Ile		
		35					40					45					
Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu		
	50					55					60						
Thr	Gln	Val	Ser	Leu	Phe	Ala	Val	Phe	Gly	Cys	Met	Glu	Asp	Met	Leu		
65					70					75					80		
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Asp	Ile	Cys	His	Pro	Leu		
				85					90					95			
Asp	Tyr	Pro	Val	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu		
			100					105					110				
Leu	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Asn	Trp	Ile		
		115					120					125					
Ala	Leu	Gln	Ile	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe		
	130					135					140						
Cys	Asp	Pro	Ser	Gln	His	Pro	Thr	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr		
145					150					155					160		
Asn	Asp	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro		
				165				170						175			
Ile	Ser	Gly	Thr	Phe	Ser	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu		
			180					185					190				
Arg	Val	Ser	Ser	Ser	Ser	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly		
		195					200					205					
Ser	His	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Gly	Phe	Gly	Gly		
	210					215					220						
Asp	Leu	Ser	Ser	Asp	Met	Ser	Ser	Tyr	Pro	Arg	Lys	Gly	Ala	Val	Ala		
225					230					235					240		
Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr		
				245				250						255			
Ser	Arg	Asn	Arg	Glu	Ile	Lys	Ser	Ala	Leu	Arg	Gln	Leu	His	Cys	Arg		
		260						265					270				
Ile	Val	Xaa	Ser	His	Phe	Leu	Ile	Ile	Cys	Ser	Ile	Pro	Ser	Val	Val		

275 280 285  
 Xaa Val Arg Lys Gly Ser Lys  
 290 295

<210> 1193  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g110 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1193  
 Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe  
 20 25 30  
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu  
 85 90 95  
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp  
 100 105 110  
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu  
 130 135 140  
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn  
 145 150 155 160  
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn  
 165 170 175  
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu  
 245 250 255  
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala  
 260 265 270  
 Val Thr Ser Val Met Tyr Thr Val Val Ile Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu  
 290 295 300  
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser  
 305 310 315 320

<210> 1194  
 <211> 318  
 <212> PRT

<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Thr Met Leu Gly Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
 85          90          95
Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp
 100          105          110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys
 115          120          125
His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
 130          135          140
Leu Val Leu Met Ser Phe Ile Leu Ser Leu Leu Asp Ser Xaa Leu His
 145          150          155          160
Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Val
 180          185          190
Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe Leu
 195          200          205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
 210          215          220
Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
 225          230          235          240
Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 245          250          255
Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val
 260          265          270
Ala Ser Val Leu Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe Ile
 275          280          285
Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu Cys
 290          295          300
Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
 305          310          315

```

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1           5           10           15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
           20           25           30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
           35           40           45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
           50           55           60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65           70           75           80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
           85           90           95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
           100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
           115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
           130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
           165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
           180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
           195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
           210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
           245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
           260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
           275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
           290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
           325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
           340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1           5           10           15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu
           20           25           30

```

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
  35                                40                                45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
  50                                55                                60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
  65                                70                                75                                80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
  85                                90                                95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
  100                                105                                110
Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val
  115                                120                                125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
  130                                135                                140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
  145                                150                                155                                160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
  165                                170                                175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
  180                                185                                190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
  195                                200                                205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
  210                                215                                220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
  225                                230                                235                                240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
  245                                250                                255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
  260                                265                                270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
  275                                280                                285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
  290                                295                                300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
  305                                310                                315                                320

```

&lt;210&gt; 1197

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g114 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1197

```

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
  1                                5                                10                                15
Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
  20                                25                                30
Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
  35                                40                                45
Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
  50                                55                                60
Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
  65                                70                                75                                80
Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
  85                                90                                95
Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
  100                                105                                110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

```

```

      115      120      125
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
 130      135      140
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
145      150      155      160
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
      165      170      175
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
      180      185      190
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
      195      200      205
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
 210      215      220
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
225      230      235      240
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
      245      250      255
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
      260      265      270
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
      275      280      285
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly
 290      295      300
Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe
305      310      315

```

&lt;210&gt; 1198

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38gl15 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1198

```

Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro
 1      5      10      15
Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr
      20      25      30
Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp
      35      40      45
Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp
      50      55      60
Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe
65      70      75      80
Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met
      85      90      95
Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser
      100      105      110
Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met
      115      120      125
Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu
      130      135      140
Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met
145      150      155      160
Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr
      165      170      175

```

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser  
 180 185 190  
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala  
 195 200 205  
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys  
 210 215 220  
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala  
 225 230 235 240  
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val  
 245 250 255  
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys  
 260 265 270  
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu  
 275 280 285  
 Leu

&lt;210&gt; 1199

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g116 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(174)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1199

Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly  
 1 5 10 15  
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe  
 20 25 30  
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys  
 35 40 45  
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Val Ile Phe  
 50 55 60  
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr  
 65 70 75 80  
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala  
 85 90 95  
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr  
 100 105 110  
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys  
 115 120 125  
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile  
 130 135 140  
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val  
 145 150 155 160  
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg  
 165 170

&lt;210&gt; 1200

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g117 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1           5           10           15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
 20           25           30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
 35           40           45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
 50           55           60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
 65           70           75           80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
 85           90           95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
 100          105          110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
 115          120          125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
 130          135          140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
 145          150          155          160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
 165          170          175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
 180          185          190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
 195          200          205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
 210          215          220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
 225          230          235          240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
 245          250          255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
 260          265          270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
 275          280          285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
 290          295          300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
 305          310          315

```

&lt;210&gt; 1201

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g118 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala  
 20 25 30  
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile  
 35 40 45  
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe  
 50 55 60  
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr  
 65 70 75 80  
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu  
 85 90 95  
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr  
 100 105 110  
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile  
 115 120 125  
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile  
 130 135 140  
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile  
 145 150 155 160  
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile  
 165 170 175  
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr  
 180 185 190  
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile  
 195 200 205  
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu  
 210 215 220  
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu  
 245 250 255  
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln  
 260 265 270  
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn  
 275 280 285  
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr  
 290 295 300  
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr  
 305 310 315

&lt;210&gt; 1202

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g119 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
 65 70 75 80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser  
 85 90 95  
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
      210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
      275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
      290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
305      310

```

&lt;210&gt; 1203

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g120 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
 1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
      20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
      50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
65      70      75      80
Met Leu Ile Asn Phe Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
      85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
      100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
      115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
      130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
145      150      155      160

```

```

Phe Ser Tyr Arg Leu Thr Phe Cys Asn Ser Asn Thr Ile His His Phe
      165                      170                      175
Xaa Cys Asp Ile Ile Pro Leu Leu Lys Ile Phe Cys Thr Asp Ser Ser
      180                      185                      190
Ile Asn Phe Pro Met Val Phe Ile Phe Ser Cys Ser Ile Gln Val Phe
      195                      200                      205
Thr Ile Gly Thr Val Leu Val Ser Tyr Thr Phe Val Leu Ser Thr Ile
      210                      215                      220
Leu Lys Lys Lys Ser Val Lys Gly Ile Arg Lys Asp Phe Ser Thr Cys
      225                      230                      235                      240
Gly Ala His Ile Leu Pro Val Ser Leu Tyr Tyr Gly Pro Leu Ala Phe
      245                      250                      255
Met Tyr Val Gly Ser Ala Ser Gln Arg Ala Asp Asp Gln Asp Met Met
      260                      265                      270
Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Ile
      275                      280                      285
Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met Phe
      290                      295                      300
Lys Gly Asn Asn Val Xaa Ile Ser Tyr Ser
      305                      310

```

&lt;210&gt; 1204

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g121 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(171)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1204

```

Cys Xaa Val Gln Val Ser Xaa Val Ala Glu Lys Tyr Xaa Xaa Ile Leu
  1          5          10          15
Phe Val Ala Leu Phe Asn Lys Thr Lys Ser Ile Cys Gln Pro Gln Asn
      20          25          30
Ile Ala Thr Pro Arg Pro Trp Ala Phe Pro Gln His Ser Phe Thr Ser
      35          40          45
Thr Ser Cys Phe Gly Gly Thr Ser Thr Gly Leu Ser Xaa Ala Val Lys
      50          55          60
Ser Pro Ile Ser Ser Val Cys Pro Leu Leu Gln Leu Leu Gln Tyr
      65          70          75          80
Pro Cys Asn Asn Ile Thr Cys Leu Xaa Asn Ala Ala Asp Arg Glu Phe
      85          90          95
Leu Ser Phe Xaa Asp Pro Leu Leu Ala Val Gly Ser Phe Thr Ile Ser
      100          105          110
Ser Cys Leu Leu Met Leu Lys Leu Ile Ser Phe Ser Ser Ser Arg Ile
      115          120          125
Ile Ala Ser Leu Leu Ser Arg Cys Pro Thr Glu Ser His Arg Ser Pro
      130          135          140
Phe Xaa Tyr Ser Phe Cys His Leu Phe Cys Leu Phe Phe Phe Met Thr
      145          150          155          160
Glu Asn Pro Trp Xaa Tyr Leu Xaa Phe Pro Ser
      165          170

```

&lt;210&gt; 1205

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g122 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1           5           10           15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
          20           25           30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
          35           40           45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
          50           55           60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
65           70           75           80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
          85           90           95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
          100          105          110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
          115          120          125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
130          135          140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
145          150          155          160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
          165          170          175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
          180          185          190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
          195          200          205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
210          215          220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
225          230          235          240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
          245          250          255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
          260          265          270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
          275          280          285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
290          295          300
Phe Phe Asn Lys
305

```

&lt;210&gt; 1206

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g123 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
          20           25           30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
          35           40           45

```

```

      100              105              110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
      115              120              125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
      130              135              140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
145              150              155              160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
      165              170              175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
      180              185              190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
      195              200              205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
210              215              220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
225              230              235              240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
      245              250              255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
      260              265              270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
275              280              285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
290              295              300
Ser Ser Val Lys
305

```

&lt;210&gt; 1208

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g125 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
      85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
180      185      190

```

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu
    195                200                205
Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys
    210                215                220
Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser
    225                230                235                240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
    245                250                255
Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr
    260                265                270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
    275                280                285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val
    290                295                300
Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu
    305                310                315                320
Ile

```

&lt;210&gt; 1209

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g126 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1209

```

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro
  1          5          10          15
Glu Thr Glu Gly Leu Glu Thr Ala Leu Phe Leu Phe Ser Ser Phe
    20          25          30
Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile
    35          40          45
Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu
    50          55          60
Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu
    65          70          75          80
Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val
    85          90          95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
    100          105          110
Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu
    115          120          125
Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr
    130          135          140
Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu
    145          150          155          160
Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe
    165          170          175
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu
    180          185          190
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys
    195          200          205
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser
    210          215          220
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser
    225          230          235          240
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile
    245          250          255
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile

```

260 265 270  
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
 275 280 285  
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro  
 290 295

<210> 1210  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g127 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 1210  
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu  
 20 25 30  
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu  
 35 40 45  
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly  
 50 55 60  
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu  
 85 90 95  
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys  
 100 105 110  
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu  
 130 135 140  
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu  
 145 150 155 160  
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His  
 165 170 175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser  
 180 185 190  
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val  
 195 200 205  
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu Ile  
 210 215 220  
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr  
 225 230 235 240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val  
 245 250 255  
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
 260 265 270  
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met  
 290 295 300  
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr  
 305 310 315 320  
 Lys Ile Phe Pro



<210> 1211  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g128 protein)

<220>  
 <223> Synthetic construct

<400> 1211  
 Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe  
 1 5 10 15  
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe  
 20 25 30  
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile  
 35 40 45  
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn  
 50 55 60  
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala  
 65 70 75 80  
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys  
 85 90 95  
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu  
 100 105 110  
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro  
 115 120 125  
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala  
 130 135 140  
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly  
 145 150 155 160  
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe  
 165 170 175  
 Phe Cys Glu Val Pro Pro Leu Leu Leu Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190  
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val  
 195 200 205  
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile  
 210 215 220  
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr  
 245 250 255  
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu  
 260 265 270  
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe  
 290 295 300  
 Pro Phe Phe Arg  
 305

<210> 1212  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g129 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
 20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
 35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
 50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
 65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
 85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145          150          155          160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
180          185          190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
195          200          205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
210          215          220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
245          250          255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
260          265          270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
290          295          300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305          310          315

```

&lt;210&gt; 1213

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g130 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
 20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
 35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
 50          55          60

```

```

Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
65          70          75          80
Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu
          85          90          95
Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
          100         105         110
Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115         120         125
Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
          130         135         140
Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
145          150         155         160
Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His
          165         170         175
Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
          180         185         190
Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
          195         200         205
Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
          210         215         220
Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
225          230         235         240
Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe
          245         250         255
Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile
          260         265         270
Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
          275         280         285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile
          290         295         300
Leu Leu Lys Ile Lys Ser Gln
305          310

```

&lt;210&gt; 1214

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g131 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1214

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
1          5          10          15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
          20         25         30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
          35         40         45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
          50         55         60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
          100         105         110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```

115	120	125
His Pro Leu Tyr	His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe	
130	135	140
Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu		
145	150	155
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile		160
	165	170
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys		175
	180	185
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe		190
	195	200
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		205
210	215	220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe		
225	230	235
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr		240
	245	250
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys		255
	260	265
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn		270
	275	280
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp		285
290	295	300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His		
305	310	315
Leu Phe His Ser Phe Cys Arg Met		320
	325	

&lt;210&gt; 1215

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g132 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1215

Met Glu Pro Gln Phe Thr Thr Gln Gly Ser Met Phe Val Leu Leu Gly	
1	5
Xaa Ser Gln Thr Gln Glu Leu Gln Arg Val Met Phe Ile Leu Phe Leu	10
	20
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr	25
	30
Val Thr Phe Asp Cys Arg Leu His Pro Met Tyr Phe Leu Leu Arg Asn	35
	40
50	55
Leu Ala Leu Ile Asp Val Cys Tyr Ser Thr Val Thr Ser Pro Lys Met	60
65	70
Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly Cys	75
	80
	85
Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val Phe	90
	95
	100
Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln Pro	105
	110
115	120
Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu Val	125
130	135
Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu Ala	140
145	150
	155
	160

```

Val Ile Arg Pro Gln Pro Leu Cys Gly Pro Asn Ile Leu Asp Asn Phe
      165                      170                      175
Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr Ser
      180                      185                      190
Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile Ile
      195                      200                      205
Trp Phe Leu Leu Ser Leu Met Ser Tyr Thr Val Ile Leu Val Met Leu
      210                      215                      220
Arg Ser His Ser Gly Lys Ala Arg Ser Lys Ala Ala Ser Thr Cys Thr
      225                      230                      235                      240
Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr Ile
      245                      250                      255
Tyr Thr Trp Pro Phe Thr Pro Phe Ile Met Asp Lys Ala Val Ser Ile
      260                      265                      270
Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr Leu
      275                      280                      285
Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys Leu
      290                      295                      300
Val Ile Cys Arg Glu Leu Thr Leu Ser Lys Leu Thr Leu Asn Asp Lys
      305                      310                      315                      320
Leu Leu Trp Ile Cys Tyr Phe Pro
      325

```

<210> 1216  
 <211> 129  
 <212> PRT  
 <213> Unknown (H38g133 protein)

<220>  
 <223> Synthetic construct

```

<400> 1216
Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
  1                      5                      10                      15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
      20                      25                      30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
      35                      40                      45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
      50                      55                      60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
      65                      70                      75                      80
Leu Leu Val Asn Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
      85                      90                      95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100                      105                      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115                      120                      125
Pro

```

<210> 1217  
 <211> 335  
 <212> PRT  
 <213> Unknown (H38g134 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Leu
 35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
 85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100         105         110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115         120         125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
 130         135         140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
 145         150         155         160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
 165         170         175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
 180         185         190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
 195         200         205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
 210         215         220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala
 225         230         235         240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245         250         255
Thr Gly Val Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 260         265         270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
 275         280         285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
 290         295         300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
 305         310         315         320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
 325         330         335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38g135 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1          5          10          15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu  
                   20                  25                  30  
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr  
                   35                  40                  45  
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
                   50                  55                  60  
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile  
                   65                  70                  75                  80  
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met  
                   85                  90                  95  
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu  
                   100                  105                  110  
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu  
                   115                  120                  125  
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val  
                   130                  135                  140  
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe  
                   145                  150                  155                  160  
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
                   165                  170                  175  
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr  
                   180                  185                  190  
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
                   195                  200                  205  
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys  
                   210                  215                  220  
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser  
                   225                  230                  235                  240  
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr  
                   245                  250                  255  
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe  
                   260                  265                  270  
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
                   275                  280                  285  
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val  
                   290                  295                  300  
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg  
                   305                  310                  315

&lt;210&gt; 1219

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g136 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly  
   1                  5                  10                  15  
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu  
                   20                  25                  30  
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys  
                   35                  40                  45  
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala  
                   50                  55                  60  
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

65					70					75					80
Gly	Phe	Leu	Arg	Arg	Gly	Thr	Ala	Leu	Pro	Val	Thr	Ser	Cys	Glu	Ala
				85					90					95	
Gln	Leu	Cys	Ser	Val	Val	Met	Phe	Gly	Thr	Ser	Glu	Cys	Phe	Leu	Leu
			100					105					110		
Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser	Pro	Leu	Val
		115					120					125			
Asn	Ser	Thr	His	Leu	Ser	Pro	Ile	Ile	Cys	Ile	Leu	Leu	Val	Gly	Val
		130				135					140				
Cys	Tyr	Leu	Gly	Gly	Trp	Val	Asn	Ala	Ser	Thr	Phe	Thr	Ser	Cys	Leu
145					150					155				160	
Leu	Ser	Leu	Ser	Phe	Cys	Gly	Pro	Asn	Gln	Ile	Asp	His	Phe	Phe	Cys
				165					170					175	
Asp	Phe	Ser	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asn	Ile	Ser	Ile	Pro
			180					185					190		
Glu	Ile	Ile	Pro	Ser	Ile	Ser	Ser	Gly	Ser	Ile	Ile	Val	Val	Thr	Val
		195					200					205			
Phe	Ala	Ile	Ala	Ile	Ser	Tyr	Ile	Tyr	Ile	Leu	Ile	Thr	Ile	Leu	Lys
	210					215					220				
Met	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr	Cys	Thr	Ser
225					230					235				240	
His	Leu	Ala	Ala	Val	Thr	Leu	Tyr	Tyr	Gly	Thr	Ile	Thr	Phe	Ile	Tyr
				245					250					255	
Val	Met	Pro	Lys	Ser	Ser	Tyr	Ser	Thr	Ser	Gln	Asn	Arg	Leu	Ile	Ser
			260					265					270		
Leu	Ser	Tyr	Thr	Val	Val	Ile	Pro	Ile	Leu	Asn	Pro	Phe	Ile	Tyr	Ser
		275					280					285			
Leu	Arg	Asn	Arg	Asp	Val	Lys	Glu	Ala	Leu	Arg	Lys	Ala	Thr	Val	Arg
	290				295						300				
Ile	Tyr	Ser	Xaa	Asp	Gln	Phe	Val								
305					310										

&lt;210&gt; 1220

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g137 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1220

His	Thr	Glu	Pro	Arg	Asn	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5				10					15		
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Leu	Leu	Ser
			20					25				30			
Leu	Ser	Leu	Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ser
		35				40						45			
Ile	Pro	Ala	Val	Ser	Ser	Asp	Ser	Pro	Leu	His	Thr	Pro	Thr	Tyr	Phe
	50				55					60					
Phe	Leu	Ser	Ile	Leu	Cys	Trp	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Ala	Thr
65				70				75						80	
Val	Ser	Lys	Thr	Ile	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Ser
			85					90					95		
His	Ala	Gly	Cys	Leu	Thr	Gln	Met	Ser	Phe	Leu	Val	Leu	Phe	Ala	Cys
		100					105					110			
Ile	Glu	Gly	Met	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Gly
	115					120						125			



```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
          245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
          260          265          270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310          315          320
Phe Phe Trp Cys

```

&lt;210&gt; 1221

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g138 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1          5          10          15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
          20          25          30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
          35          40          45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
          50          55          60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Asp Ile Val Leu
65          70          75          80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
          85          90          95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
          100          105          110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
          115          120          125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
          130          135          140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145          150          155          160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
          165          170          175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
          180          185          190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

	195					200					205						
Ala	Gly	Trp	Thr	Leu	Leu	Gly	Ser	Asp	Leu	Phe	Leu	Ile	Phe	Leu	Ser		
	210					215					220						
Tyr	Thr	Phe	Ile	Leu	Arg	Ala	Val	Leu	Arg	Phe	Lys	Ala	Glu	Gly	Ala		
225					230					235					240		
Ala	Val	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Phe	Ile	Leu	Ile	Leu		
				245					250					255			
Phe	Phe	Ser	Thr	Ile	Leu	Leu	Val	Val	Val	Leu	Thr	Asn	Val	Ala	Arg		
			260					265					270				
Lys	Lys	Val	Pro	Met	Asp	Ile	Leu	Ile	Leu	Leu	Asn	Val	Leu	His	His		
	275					280						285					
Leu	Ile	Pro	Pro	Ala	Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val	Arg	Thr	Lys		
	290					295					300						
Glu	Ile	Lys	Gln	Gly	Ile	Gln	Lys	Leu	Leu	Gln	Arg	Gly	Arg				
305					310					315							

&lt;210&gt; 1222

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g139 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(236)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1222

Pro	Lys	Val	Pro	Asp	Phe	Phe	Val	Phe	Gly	Leu	Arg	Ala	Ile	Ser	Phe		
1				5					10					15			
Pro	Ala	Gly	Phe	Leu	Gln	Lys	Tyr	Ile	Lys	Asn	Cys	Phe	Gln	Ala	Met		
		20						25					30				
Glu	Phe	Trp	Pro	Phe	Lys	Val	Arg	Ala	Met	Asp	Arg	Xaa	Gly	Thr	Leu		
	35					40					45						
Cys	His	Pro	Leu	Lys	Tyr	Pro	Ser	Ile	Ile	Thr	Asp	Pro	Phe	Gly	Val		
	50					55				60							
Lys	Ala	Ala	Arg	Phe	Ile	Leu	Pro	Arg	Asn	Val	Leu	Met	Thr	Leu	Pro		
65					70				75					80			
Ile	Pro	Ile	Leu	Ser	Ala	Gln	Leu	Arg	Tyr	Cys	Gly	Arg	Asn	Val	Ile		
			85					90					95				
Glu	Asn	Cys	Ile	Cys	Ala	Asn	Met	Ser	Val	Ser	Arg	Leu	Ser	Cys	Asp		
	100						105					110					
Asp	Val	Thr	Ile	Asn	His	Leu	Tyr	Gln	Phe	Ala	Gly	Gly	Trp	Thr	Leu		
	115					120						125					
Leu	Gly	Ser	Asp	Leu	Ile	Leu	Ile	Phe	Leu	Ser	Tyr	Thr	Phe	Ile	Leu		
	130					135					140						
Arg	Ala	Val	Leu	Arg	Leu	Lys	Ala	Glu	Gly	Ala	Val	Ala	Lys	Ala	Leu		
145					150				155					160			
Ser	Thr	Cys	Gly	Ser	His	Phe	Met	Leu	Ile	Leu	Phe	Phe	Ser	Thr	Ile		
			165					170						175			
Leu	Leu	Val	Phe	Val	Leu	Thr	His	Val	Ala	Lys	Lys	Lys	Val	Ser	Pro		
	180						185						190				
Asp	Val	Pro	Val	Leu	Leu	Asn	Val	Leu	His	His	Val	Ile	Pro	Ala	Ala		
	195					200						205					
Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Arg	Thr	Gln	Glu	Ile	Lys	Gln	Gly		
	210					215					220						
Met	Gln	Arg	Leu	Leu	Lys	Lys	Gly	Cys	Xaa	Gln	Gly						
225					230					235							

&lt;210&gt; 1223

<211> 308  
 <212> PRT  
 <213> Unknown (H38g140 protein)

<220>  
 <223> Synthetic construct

<400> 1223  
 Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile  
 1 5 10 15  
 Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met  
 20 25 30  
 Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Ile Leu Ile Arg Ile Ser  
 35 40 45  
 Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe  
 50 55 60  
 Ala Asp Met Ala Tyr Ser Ser Val Thr Pro Asn Met Leu Val Asn  
 65 70 75 80  
 Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln  
 85 90 95  
 Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala  
 100 105 110  
 Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr  
 115 120 125  
 Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Leu Val Val  
 130 135 140  
 Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr  
 145 150 155 160  
 Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp  
 165 170 175  
 Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr  
 180 185 190  
 Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys  
 195 200 205  
 Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met  
 210 215 220  
 Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His  
 225 230 235 240  
 Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val  
 245 250 255  
 Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val  
 260 265 270  
 Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
 275 280 285  
 Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys  
 290 295 300  
 Ile Leu Ser His  
 305

<210> 1224  
 <211> 335  
 <212> PRT  
 <213> Unknown (H38g141 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(335)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
 35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
 85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
115          120          125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
130          135          140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
165          170          175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
180          185          190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
195          200          205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
245          250          255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
290          295          300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
325          330          335

```

&lt;210&gt; 1225

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g142 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
 1          5          10          15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
 20          25          30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
 35          40          45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
 50          55          60

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val  
 65 70 75 80  
 Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly  
 85 90 95  
 Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu  
 130 135 140  
 Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile  
 145 150 155 160  
 Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His  
 165 170 175  
 Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp  
 180 185 190  
 Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val  
 195 200 205  
 Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr  
 210 215 220  
 Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr  
 245 250 255  
 Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys  
 260 265 270  
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu  
 290 295 300  
 Leu Arg Ile Lys Ile Phe Ser  
 305 310

&lt;210&gt; 1226

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g143 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1226

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu  
 1 5 10 15  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr  
 65 70 75 80  
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly  
 85 90 95  
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser  
 100 105 110  
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile  
 130 135 140  
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

&lt;210&gt; 1227

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g144 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ser Ile Gly Pro Lys
65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Tyr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser  
 210 215 220  
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr  
 225 230 235 240  
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe  
 245 250 255  
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn  
 260 265 270  
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys  
 290 295 300  
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser  
 305 310 315

&lt;210&gt; 1228

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g145 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe  
 1 5 10 15  
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser  
 20 25 30  
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr  
 35 40 45  
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr  
 50 55 60  
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr  
 65 70 75 80  
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile  
 85 90 95  
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu  
 100 105 110  
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe  
 130 135 140  
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr  
 145 150 155 160  
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Leu Gly Thr Met Phe  
 165 170 175  
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp  
 180 185 190  
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys  
 195 200

&lt;210&gt; 1229

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g146 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
 20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
 65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
 85          90          95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100         105         110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115         120         125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
 130         135         140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145         150         155         160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165         170         175
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
 180         185         190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
 195         200

```

&lt;210&gt; 1230

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g147 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1          5          10          15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20          25          30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35          40          45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50          55          60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
 65          70          75          80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
 85          90          95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
 100         105         110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115         120         125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130         135         140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile
 145         150         155         160
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
 165         170         175

```



```

Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180                      185                      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195                      200                      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210                      215                      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245                      250                      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260                      265                      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275                      280                      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290                      295                      300

```

&lt;210&gt; 1231

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g148 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(110)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1231

```

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1          5          10          15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20          25          30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35          40          45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50          55          60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65          70          75          80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85          90          95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100          105          110

```

&lt;210&gt; 1232

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g149 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1232

```

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1          5          10          15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```
<210> 1233
<211> 241
<212> PRT
<213> Unknown (H38g150 protein)
```

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(241)
<223> Xaa = Any Amino Acid
```

<400> 1233															
Leu	Arg	Gln	Leu	His	Asn	Leu	Phe	Leu	Pro	Val	Gly	Phe	Phe	Leu	Ser
1				5					10					15	
Ser	Tyr	Ser	Phe	Xaa	Val	Ile	Trp	His	Asn	Leu	Asn	Ser	Val	Thr	Lys
			20					25					30		
Phe	Ser	Ser	Lys	Thr	Asp	Glu	Ser	Lys	Leu	Lys	Ser	Xaa	Cys	Lys	Val
		35					40					45			
Lys	Ser	Leu	Phe	Phe	Thr	Tyr	Ala	Gly	Cys	Cys	Glu	Lys	Leu	Leu	Leu
	50					55					60				

Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu  
65 70 75 80  
His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val  
85 90 95  
Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys  
100 105 110  
Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu  
115 120 125  
Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro  
130 135 140  
Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro  
145 150 155 160  
His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser  
165 170 175  
Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly  
180 185 190  
Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val  
195 200 205  
Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val  
210 215 220  
Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly  
225 230 235 240  
Pro

&lt;210&gt; 1234

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g151 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu  
1 5 10 15  
Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu  
20 25 30  
Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu  
35 40 45  
Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr  
50 55 60  
Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val  
65 70 75 80  
Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser  
85 90 95  
Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr  
100 105 110  
Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala  
115 120 125  
Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val  
130 135 140  
Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu  
145 150 155 160  
Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile  
165 170 175  
Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys  
180 185 190  
Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr  
195 200 205  
Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile

```

      210                215                220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225                230                235                240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245                250                255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260                265                270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275                280                285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290                295                300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305                310

```

<210> 1235  
 <211> 135  
 <212> PRT  
 <213> Unknown (H38g152 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(135)  
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1                5                10                15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20                25                30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35                40                45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50                55                60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
      65                70                75                80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85                90                95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100               105               110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115               120               125
Arg Arg Leu Xaa Lys Ile Lys
      130               135

```

<210> 1236  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g153 protein)

<220>  
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1                5                10                15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Cys
      20                25                30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35                40                45

```

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50          55          60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65          70          75          80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
      85          90          95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
      100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
      115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
      130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
      165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
      180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
      195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
      210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
      245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
      260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
      275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
      290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
305          310          315

```

&lt;210&gt; 1237

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g154 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1237

```

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20          25          30
Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
      35          40          45
Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
      50          55          60
Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
65          70          75          80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
      85          90          95
Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

```

&lt;210&gt; 1238

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g155 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1238

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser  
 180 185 190  
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr  
 195 200 205  
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg  
 210 215 220  
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr  
 245 250 255  
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met  
 260 265 270  
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu  
 275 280 285  
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val  
 290 295 300  
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu  
 305 310 315

&lt;210&gt; 1239

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g156 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
 65 70 75 80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser  
 85 90 95  
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile  
 115 120 125  
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala  
 130 135 140  
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro  
 145 150 155 160  
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser  
 180 185 190  
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu  
 195 200 205  
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys  
 210 215 220  
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

```

225          230          235          240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
          245          250          255
Ile Asn Leu Ala Val Val His Arg Phe Ala Arg His Val Ser Pro Leu
          260          265          270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Val Pro Pro Leu Thr
          275          280          285
Asn Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
          290          295          300
Val Ala Lys Leu Cys Gln Arg Lys Ile
305          310

```

&lt;210&gt; 1240

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g157 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1240

```

Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu Ser
          50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu Leu
          100          105          110
Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu His
          115          120          125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
          130          135          140
Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe Ile
145          150          155          160
Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met Trp
          165          170          175
Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr Leu
          180          185          190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
          195          200          205
Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg Thr
          210          215          220
His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser His
225          230          235          240
Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
          245          250          255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
          260          265          270
Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
          290          295          300
Ser Ser Val Lys
305

```



<210> 1241  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g158 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 1241  
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe  
 1 5 10 15  
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu  
 20 25 30  
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile  
 35 40 45  
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr  
 50 55 60  
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser  
 65 70 75 80  
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn  
 85 90 95  
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly  
 100 105 110  
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu  
 130 135 140  
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu  
 145 150 155 160  
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile  
 165 170 175  
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys  
 180 185 190  
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe  
 195 200 205  
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu  
 210 215 220  
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro  
 245 250 255  
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His  
 260 265 270  
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser  
 275 280 285  
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg  
 290 295 300  
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu  
 305 310 315 320  
 Leu

<210> 1242  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g159 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(162)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1242

```

Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asp Pro
 1           5           10           15
Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Leu Leu Lys Leu
      20           25           30
Leu Cys Met Gly Thr Thr Asn Thr Leu Gly Phe Phe Val Ala Ala Asn
      35           40           45
Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa
      50           55           60
Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu Arg Cys
      65           70           75           80
Lys Ala Leu Ser Thr Cys Ile Ser His Thr Thr Val Val Ile Leu Phe
      85           90           95
Phe Gly Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu Leu Pro
      100          105          110
Ile Asn Lys Ala Val Ala Val Phe Tyr Thr Met Ile Asn Pro Met Leu
      115          120          125
Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Ala Leu
      130          135          140
Arg Lys Leu Trp Val Lys Arg Xaa Thr Glu Glu Arg Asn Asn Pro Asn
      145          150          155          160
Ile Arg

```

&lt;210&gt; 1243

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g160 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1243

```

Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro
      20           25           30
Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu
      35           40           45
Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe
      50           55           60
Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Ala Thr Ser Val
      65           70           75           80
Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr
      85           90           95
Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met
      100          105          110
Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Leu Val Leu Val
      130          135          140
Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro
      145          150          155          160

```

```

Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile
                165                170                175
Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly
                180                185                190
Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe
                195                200                205
Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg
                210                215                220
Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser
                225                230                235
Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser
                245                250                255
Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr
                260                265                270
Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu
                275                280                285
Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
                290                295                300
Leu Tyr Val Phe Thr Lys Lys
305                310

```

&lt;210&gt; 1244

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g161 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1244

```

Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
  1                5                10                15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
                20                25                30
Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr
                35                40                45
Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu
                50                55                60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
                65                70                75                80
Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met
                85                90                95
Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu
                100                105                110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
                115                120                125
His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly
                130                135                140
Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
                145                150                155                160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
                165                170                175
Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met
                180                185                190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
                195                200                205
Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

```

210		215		220
Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser				
225		230		235
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr				240
	245		250	255
Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe				
	260	265		270
Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg				
	275	280		285
Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp				
	290	295	300	
Ile Ser Gly Asn Lys Xaa Met Xaa Leu Glu Leu				
305	310		315	

&lt;210&gt; 1245

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g162 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1245

Ser Asn Thr Gly Met Ser Ile Leu Asn Thr Ser Glu Met Glu Ile Ser				
1	5	10	15	
Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp				
	20	25	30	
Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn				
	35	40	45	
Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro				
	50	55	60	
Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser				
	65	70	75	80
Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro				
	85	90	95	
Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly				
	100	105	110	
Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg				
	115	120	125	
Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser				
	130	135	140	
Ala Arg Val Ile Gln Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu				
	145	150	155	160
Leu Ile Leu Pro Phe Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys				
	165	170	175	
Lys Asn Leu Leu Ser Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys				
	180	185	190	
Leu Ala Cys Thr Asp Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val				
	195	200	205	
Ala Leu Thr Gly Ile Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met				
	210	215	220	
Leu Ile Leu Lys Ala Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu				
	225	230	235	240
Lys Val Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe				
	245	250	255	
Tyr Val Pro Ile Ile Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His				
	260	265	270	

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val  
 275 280 285  
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile  
 290 295 300  
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly  
 305 310 315 320  
 Cys Leu

&lt;210&gt; 1246

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g163 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu  
 1 5 10 15  
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu  
 20 25 30  
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile  
 35 40 45  
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys  
 100 105 110  
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu  
 145 150 155 160  
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

&lt;210&gt; 1247

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g164 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1247

```

Met Arg Leu Ile Xaa Asp Glu Glu Met Ser Arg Arg Asn Tyr Thr Glu
 1           5           10           15
Leu Thr Glu Phe Val Leu Leu Gly Leu Thr Ser Arg Pro Glu Leu Arg
      20           25           30
Val Ala Phe Leu Ala Leu Phe Leu Phe Val Tyr Ile Ala Thr Val Val
      35           40           45
Gly Asn Leu Gly Met Ile Ile Leu Ile Lys Val Asp Ser Arg Leu His
      50           55           60
Thr Pro Met Xaa Phe Phe Leu Ser Ser Leu Ser Ile Leu Asp Leu Cys
65           70           75           80
Phe Ser Thr Asn Phe Thr Pro Lys Met Leu Glu Asn Phe Leu Ser Glu
      85           90           95
Lys Lys Thr Ile Ser Tyr Ala Gly Cys Leu Met Gln Cys Tyr Val Val
      100          105          110
Ile Ala Val Val Leu Ala Glu His Cys Met Leu Ala Val Met Ala Tyr
      115          120          125
Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met
      130          135          140
Ser Gln Gly Val Cys Val His Leu Val Ile Val Pro Tyr Val Tyr Gly
145          150          155          160
Phe Leu Leu Ser Val Met Glu Thr Leu Arg Thr Tyr Asn Leu Ser Phe
      165          170          175
Cys Gly Thr Asn Glu Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu
      180          185          190
Ile Lys Leu Ala Cys Ser Asp Thr Tyr Ser Lys Glu Leu Ser Met Tyr
      195          200          205
Ile Val Ala Gly Tyr Ser Asn Val Gln Ser Leu Leu Ile Ile Leu Thr
      210          215          220
Ser Tyr Met Phe Ile Leu Val Ala Ile Leu Arg Ser His Ser Ala Glu
225          230          235          240
Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val
      245          250          255
Thr Ile Phe Tyr Gly Thr Leu Phe Cys Met His Leu Arg Arg Pro Thr
      260          265          270
Asp Glu Ser Val Glu Gln Gly Lys Met Val Ala Val Phe Tyr Thr Thr
      275          280          285
Val Ile Leu Met Leu Asn Ser Met Ile Tyr Gly Leu Arg Asn Lys Asp
      290          295          300
Val Lys Glu Ala Leu Lys Lys Ala Ile Gly Lys Gln Thr Leu Gly Lys
305          310          315          320

```

&lt;210&gt; 1248

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g165 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1248

```

Arg Arg Met Gly Asn His Thr Ala Val Ser Leu Phe Leu Leu Trp Gly
 1      5      10      15
Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
 20      25      30
Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
 35      40      45
Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50      55      60
Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Val Ile Pro Arg
 65      70      75      80
Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
 85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
 100     105     110
Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
 115     120     125
Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
 130     135     140
Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
 145     150     155     160
Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
 165     170     175
Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
 180     185     190
Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
 195     200     205
Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
 210     215     220
Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
 225     230     235     240
Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
 245     250     255
Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
 260     265     270
Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
 275     280     285
Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
 290     295     300
Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
 305     310     315

```

&lt;210&gt; 1249

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g166 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1249

```

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
 1      5      10      15
Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
 20      25      30
Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
 35      40      45
Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

```

50	55	60
Leu Cys Met Leu Ala Val Val Asp Leu Val Val Cys Ser Thr Ala Val		
65	70	75
Pro Lys Leu Leu Ser Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe		80
	85	90
Glu Thr Cys Leu Thr Gln Met Phe Leu Ile His Ser Cys Ser Thr Met		95
	100	105
Glu Ser Gly Phe Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile		110
	115	120
Cys Asn Pro Leu Arg His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly		125
	130	135
Arg Val Gly Leu Ala Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro		140
	145	150
His Ser Phe Leu Leu Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile		155
	165	170
Ser His Thr Tyr Cys Glu Phe Met Ala Leu Ile Arg Ile Ala Cys Ala		175
	180	185
Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile Val Ala Phe Leu Thr		190
	195	200
Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser Tyr Val Leu Ile Leu		205
	210	215
His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala Arg Leu Lys Ser Leu		220
	225	230
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Val Ser Tyr Thr Pro		235
	245	250
Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Ala Pro		255
	260	265
His Phe His Ile Phe Val Ala Asn Ile Tyr Leu Leu Val Pro Pro Met		270
	275	280
Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Arg Ile Trp Asp Arg		285
	290	295
Phe Leu Lys Val Phe Ser Phe Ser Lys Pro Leu Ser Lys Ser Phe		300
	310	315

&lt;210&gt; 1250

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g167 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1250

Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr	
1	5
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val	10
	20
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys	25
	30
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu	35
	40
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu	45
	50
Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu	55
	60
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile	65
	70
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu	75
	80
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140



Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp  
 145 150 155 160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr  
 165 170 175  
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val  
 180 185 190  
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser  
 195 200 205  
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu  
 210 215 220  
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met  
 245 250 255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
 260 265 270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser  
 290 295 300  
 Arg Ser Cys  
 305

&lt;210&gt; 1251

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g168 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe  
 1 5 10 15  
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe  
 20 25 30  
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu  
 35 40 45  
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr  
 50 55 60  
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val  
 65 70 75 80  
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val  
 85 90 95  
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu  
 100 105 110  
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg  
 130 135 140  
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His  
 145 150 155 160  
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro  
 165 170 175  
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu  
 180 185 190  
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile  
 195 200 205  
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile  
 210 215 220  
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

```

225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

```

&lt;210&gt; 1252

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g169 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1252

```

Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
          65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
          130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
          145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
          210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Ser Val Glu Gln Gly Lys
          260          265          270

```

Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val  
 290 295 300  
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Phe  
 305 310 315 320  
 Val Phe

<210> 1253

<211> 311

<212> PRT

<213> Unknown (H38g170 protein)

<220>

<223> Synthetic construct

<400> 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro  
 1 5 10 15  
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val  
 20 25 30  
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg  
 35 40 45  
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu  
 50 55 60  
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu  
 65 70 75 80  
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys  
 85 90 95  
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe  
 100 105 110  
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro  
 115 120 125  
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala  
 130 135 140  
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile  
 145 150 155 160  
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr  
 165 170 175  
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser  
 180 185 190  
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly  
 195 200 205  
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile  
 210 215 220  
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys  
 225 230 235 240  
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val  
 245 250 255  
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala  
 260 265 270  
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys  
 290 295 300  
 Val Ala His Pro Gln Arg Lys  
 305 310

<210> 1254

<211> 320

<212> PRT  
 <213> Unknown (H38g171 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1254  
 Gly Val Gly Leu Xaa Lys Leu Xaa Trp Gln Ile Ile Phe Ser Gly Asp  
 1 5 10 15  
 Ser Phe Ser Thr Trp Glu Met Phe Ser Leu Ser Ile Leu Gln Leu Pro  
 20 25 30  
 Xaa Met Tyr Thr Val Ala Leu Ser Gly Thr Ser Ile Leu Ile Phe Leu  
 35 40 45  
 Ile Xaa Thr Asp Phe Xaa Val His Thr Ser Leu Tyr Ser Phe Xaa Val  
 50 55 60  
 Leu Ile Asp Ile Ala Ile Ser Val Val Lys Ile Gly Ile Glu Val Phe  
 65 70 75 80  
 Ser Gly Lys Ile Asn Phe Ser His Thr Gly Cys Gly Thr Gln Ile Phe  
 85 90 95  
 Phe Phe Leu Thr Ala Gly Ile Phe Lys Tyr Val Leu Leu Thr Tyr Met  
 100 105 110  
 Ala Tyr Asp His Asn Val Ala Ile Cys Asp Leu Arg Xaa Pro Thr Phe  
 115 120 125  
 Met Ser Asp Gln Val Phe Xaa Gln Trp Ala Val Glu Ser Trp Ile Gly  
 130 135 140  
 Gly Lys Leu Ser Ser Leu Ala His Thr Ile Tyr Ile Phe His Leu Phe  
 145 150 155 160  
 Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa  
 165 170 175  
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr  
 180 185 190  
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser  
 195 200 205  
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly  
 210 215 220  
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile  
 225 230 235 240  
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe  
 245 250 255  
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu  
 260 265 270  
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val  
 275 280 285  
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln  
 290 295 300  
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser  
 305 310 315 320

<210> 1255  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g172 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1           5           10           15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
 20           25           30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
 35           40           45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
 50           55           60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
 65           70           75           80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
 85           90           95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
100           105           110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
115           120           125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
130           135           140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
145           150           155           160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
165           170           175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
180           185           190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
195           200           205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
210           215           220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
225           230           235           240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
245           250           255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
260           265           270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
275           280           285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
290           295           300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
305           310           315           320

```

&lt;210&gt; 1256

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g173 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(235)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1           5           10           15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

	20		25		30										
Ala	Leu	Asp	Ala	Pro	Leu	Phe	Gly	Val	Phe	Leu	Val	Val	Tyr	Val	Leu
	35		40		45										
Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Val	Ile	Arg	Val	Tyr	Ser
	50		55		60										
His	Leu	His	Thr	Pro	Lys	Tyr	Tyr	Phe	Leu	Thr	Asn	Leu	Ser	Phe	Ile
	65		70		75										
Asp	Leu	Trp	Phe	Phe	Thr	Val	Met	Val	Pro	Lys	Met	Pro	Arg	Thr	Leu
			85		90										
Leu	Ser	Leu	Cys	Gly	Lys	Ala	Val	Ser	Phe	His	Ser	Cys	Met	Thr	Gln
			100		105										
Leu	Tyr	Phe	Phe	Tyr	Phe	Leu	Gly	Ser	Thr	Glu	Cys	Leu	Leu	Tyr	Thr
			115		120										
Val	Met	Ser	Tyr	Asp	Arg	Tyr	Arg	Gly	Asn	Thr	Gln	His	Phe	Pro	Gly
			130		135										
Ser	Glu	Asn	Leu	Pro	Thr	Lys	Xaa	Ala	Lys	Cys	Xaa	Trp	Pro	Gly	Gly
			145		150										
His	Thr	Gly	Leu	Pro	Leu	Ile	Ile	Leu	Ala	Asp	Leu	Ser	Gly	Xaa	Leu
			165		170										
Arg	Val	Asp	Ser	Ser	Xaa	Trp	Ala	Ile	Gln	Asn	Xaa	Xaa	Tyr	Asn	Leu
			180		185										
Val	Ile	Gln	Val	Lys	Phe	Ile	Thr	Cys	Ile	Gly	Leu	Ser	Ile	Lys	His
			195		200										
Tyr	Ser	Lys	Gln	Leu	Ala	Gln	Leu	Xaa	Phe	Phe	His	Arg	Leu	Ser	Lys
			210		215										
Thr	Phe	Leu	Asn	Ser	Gln	Leu	Asp	Phe	Tyr	Leu					
			225		230										

&lt;210&gt; 1257

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g174 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1257

Met	Ile	Thr	Glu	Phe	Ile	Leu	Ile	Gly	Phe	Ser	Asn	Leu	Gly	Asp	Leu
1			5					10					15		
Gln	Ile	Leu	Leu	Phe	Phe	Ile	Phe	Leu	Val	Tyr	Leu	Thr	Thr	Leu	
			20					25				30			
Met	Ala	Asn	Thr	Thr	Ile	Met	Thr	Val	Ile	His	Leu	Asp	Arg	Ala	Leu
			35				40					45			
His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Val	Leu	Ser	Cys	Ser	Glu	Thr
			50			55					60				
Cys	Tyr	Thr	Leu	Val	Ile	Val	Pro	Lys	Met	Leu	Thr	Asn	Leu	Leu	Ser
			65			70				75				80	
Ala	Ile	Pro	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Val	Val	Gln	Leu	Tyr	Leu
			85					90				95			
Phe	Val	Gly	Leu	Ala	Cys	Thr	Asn	Cys	Phe	Leu	Ile	Ala	Val	Met	Gly
			100				105					110			
Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro	Leu	Asn	Tyr	Thr	Leu	Ile
			115			120						125			
Val	Ser	Xaa	Ala	Thr	Cys	Met	Gln	Leu	Val	Leu	Ala	Ser	Ser	Phe	Cys
			130			135						140			
Gly	Phe	Leu	Thr	Ser	Val	Ile	Val	Asn	Ile	Leu	Val	Phe	Ser	Val	Leu
			145			150				155					160

```

Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
      165      170      175
Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
      180      185      190
Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
      195      200      205
Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
      210      215      220
Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
225      230      235      240
Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      245      250      255
Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
      260      265      270
Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
      275      280      285
Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
      290      295      300
Lys Thr Val
305

```

<210> 1258  
 <211> 157  
 <212> PRT  
 <213> Unknown (H38g175 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(157)  
 <223> Xaa = Any Amino Acid

```

<400> 1258
Ile Cys His Asn Arg Lys Val Ile Pro Ala Ser Met Xaa Asn Met Cys
  1      5      10      15
Xaa Phe Leu Leu Lys Val Ala Xaa Asp Asn Phe Leu His Val Leu Phe
      20      25      30
Ile Leu Ala Lys Thr Ala Pro Pro Leu Leu Phe Leu Xaa Glu Ile Pro
      35      40      45
Ser Tyr Phe Ser Ser Pro Ser Xaa Ile Ile Val Leu Xaa Cys Leu Pro
      50      55      60
Xaa Phe Leu Lys Gln Leu Val Ile Leu Phe Val Phe Leu Leu Leu Asn
      65      70      75      80
Xaa Ser Tyr Leu Thr Leu Ile Phe Met Leu Leu Thr Met Lys Ile Thr
      85      90      95
Ser Ser Phe Lys Ala Ser Thr Val Ile Ser Cys Leu Gln Phe Pro Ser
      100      105      110
Lys Ala Thr Cys Met His Gly Val Phe Ser Ala Val Cys Ala Gln Met
      115      120      125
Xaa Pro Tyr Tyr Asn Gly Xaa Ile Ile Xaa His Pro Glu Ser Ile Thr
      130      135      140
Glu Ser Lys Xaa Leu Thr Cys Val Asn Pro Xaa Phe Asn
145      150      155

```

<210> 1259  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g176 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1259

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
          20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr
          35           40           45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
          50           55           60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
65           70           75           80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
          85           90           95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
          100          105          110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
          115          120          125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
          130          135          140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
145          150          155          160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
          165          170          175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
          180          185          190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
          195          200          205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
          210          215          220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
225          230          235          240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
          245          250          255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
          260          265          270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
          275          280          285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
          290          295          300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
305          310          315          320
Pro

```

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid



&lt;400&gt; 1260

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1           5           10           15
Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
          20           25           30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
          35           40           45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
          50           55           60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
          65           70           75           80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
          85           90           95
Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
          100          105          110
Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
          130          135          140
Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
          145          150          155          160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
          165          170          175
Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
          180          185          190
Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
          195          200          205
Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
          210          215          220
Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
          225          230          235          240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
          245          250          255
Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
          260          265          270
Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
          290          295          300
Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu
          305          310          315

```

&lt;210&gt; 1261

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g178 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1261

```

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1           5           10           15
Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
          20           25           30
Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

```

<400> 1262															
Met	Arg	Gly	Phe	Asn	Lys	Thr	Thr	Val	Val	Thr	Gln	Phe	Ile	Leu	Val
1				5					10					15	
Gly	Phe	Ser	Ser	Leu	Gly	Glu	Leu	Gln	Leu	Leu	Leu	Phe	Val	Ile	Phe
			20					25					30		
Leu	Leu	Leu	Tyr	Leu	Thr	Ile	Leu	Val	Ala	Asn	Val	Thr	Ile	Met	Ala
			35				40					45			
Val	Ile	Arg	Phe	Ser	Trp	Thr	Leu	His	Thr	Pro	Met	Tyr	Gly	Phe	Leu
	50					55					60				
Phe	Ile	Leu	Ser	Phe	Ser	Glu	Ser	Cys	Tyr	Thr	Phe	Val	Ile	Ile	Pro
65					70					75					80
Gln	Leu	Leu	Val	His	Leu	Leu	Ser	Asp	Thr	Lys	Thr	Ile	Ser	Phe	Met
				85					90					95	
Ala	Cys	Ala	Thr	Gln	Leu	Phe	Phe	Phe	Leu	Gly	Phe	Ala	Cys	Thr	Asn
			100					105					110		
Cys	Leu	Leu	Ile	Ala	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
			115				120					125			

```

His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
 130                      135                      140
Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
145                      150                      155                      160
Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
                      165                      170                      175
His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
                      180                      185                      190
Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
                      195                      200                      205
Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
210                      215                      220
Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
225                      230                      235                      240
Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
                      245                      250                      255
Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
260                      265                      270
Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
275                      280                      285
Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val
290                      295                      300
Leu Gly Met Pro Val Ala Thr Lys Met Ser
305                      310

```

&lt;210&gt; 1263

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g180 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1263

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
20      25      30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
35      40      45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
50      55      60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
65      70      75      80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
85      90      95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
100     105     110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
115     120     125
Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
130     135     140
Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145     150     155     160
Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
165     170     175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
180     185     190
Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
195     200     205
Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser

```

210	215	220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		240
	245	250
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr		255
	260	265
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val		285
	290	295
Ile His Gln Lys Lys Thr Phe Phe Ser Leu		300
305	310	

&lt;210&gt; 1264

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g181 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(275)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1264

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe		
1	5	10
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val		15
	20	25
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile		30
	35	40
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His		45
	50	55
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met		60
65	70	75
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala		80
	85	90
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu		95
	100	105
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val		110
	115	120
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg		125
	130	135
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe		140
145	150	155
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg		160
	165	170
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val		175
	180	185
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr		190
	195	200
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu		205
	210	215
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro		220
225	230	235
Ser His Leu Ala Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg		240
	245	250
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val		255
	260	265
		270

Gln Tyr Ser  
275

<210> 1265

<211> 312

<212> PRT

<213> Unknown (H38g182 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1265

```

Met Arg Arg Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1           5           10          15
Thr Asn His Gln Glu Leu Gln Ile Leu Leu Phe Met Leu Phe Leu Ala
      20           25           30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Ser Met Ile Ala Leu Ile
      35           40           45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
      50           55           60
Leu Ser Phe Leu Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
      65           70           75           80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys
      85           90           95
Leu Val Gln Cys Tyr Leu Tyr Ile Ile Leu Val His Val Glu Ile Tyr
      100          105          110
Ile Leu Ala Val Met Ala Phe Asp Xaa Tyr Met Ala Ile Xaa Asn Pro
      115          120          125
Leu Leu Tyr Gly Ser Lys Met Ser Lys Ser Val Cys Ser Phe Leu Ile
      130          135          140
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
      145          150          155          160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe
      165          170          175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
      180          185          190
Asn Lys Glu Leu Ser Met Phe Val Val Ala Gly Trp Asn Leu Ser Phe
      195          200          205
Ser Leu Phe Ile Ile Phe Ile Ser Tyr Phe Tyr Ile Phe Pro Ala Ile
      210          215          220
Leu Arg Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
      225          230          235          240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe
      245          250          255
Met Cys Leu Arg Pro Pro Ser Glu Glu Ser Met Glu Gln Gly Gln Met
      260          265          270
Val Ala Val Leu Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ser Lys Glu Leu
      290          295          300
Phe Lys Arg Lys Leu Phe Pro Lys
305          310

```

<210> 1266

<211> 315

<212> PRT

<213> Unknown (H38g183 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1          5          10          15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
          20          25          30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
          35          40          45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
          50          55          60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65          70          75          80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
          85          90          95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
          100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
          115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
          130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
          165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
          180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
          195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
          210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
          245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
          260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
          290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
305          310          315

```

&lt;210&gt; 1267

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g184 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1267

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
          20          25          30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
          35          40          45

```

```

Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
 50          55          60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
 65          70          75          80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val
          85          90          95
Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu
          100          105          110
Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
          130          135          140
Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
          145          150          155          160
Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
          165          170          175
Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
          180          185          190
Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
          195          200          205
Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
          210          215          220
Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
          225          230          235          240
Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
          245          250          255
Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
          260          265          270
Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
          275          280          285
Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
          290          295          300
Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
          305          310          315

```

&lt;210&gt; 1268

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g185 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1268

```

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr
 1          - 5          10          15
Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile
          20          25          30
Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu
          35          40          45
Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu
          50          55          60
His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr
          65          70          75          80
Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
          85          90          95
Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
          100          105          110
Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
          115          120          125
Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

```

130		135		140	
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Ala Cys Ala Ile Gly					
145		150		155	160
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro					
	165		170		175
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala					
	180		185		190
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile					
	195		200		205
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys					
	210		215		220
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala					
225		230		235	240
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val					
	245		250		255
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr					
	260		265		270
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr					
	275		280		285
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys					
	290		295		300
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu					
305		310		315	320
Lys Leu Tyr Asn					

&lt;210&gt; 1269

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g186 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1269

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile		
1	5	10
Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Phe		
	20	25
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val		
	35	40
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu		
	50	55
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro		
65	70	75
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu		
	85	90
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu		
	100	105
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr		
	115	120
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro		
	130	135
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His		
145	150	155
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg		
	165	170
		175



```

His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
      180      185      190
Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
      195      200      205
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
      210      215      220
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
      225      230      235      240
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
      245      250      255
Leu Phe Met Tyr Val Arg Pro Ser Ser Tyr Thr Ser Asp Asn Asp
      260      265      270
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
      290      295      300
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
      305      310      315      320
Val Lys Leu Gln Ile Ile Leu
      325

```

&lt;210&gt; 1270

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g187 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1270

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1      5      10      15
Leu Ser Lys Pro Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
      20      25      30
Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
      35      40      45
Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
      50      55      60
Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
      65      70      75      80
Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
      85      90      95
Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
      100      105      110
Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
      115      120      125
Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
      130      135      140
Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
      145      150      155      160
Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
      165      170      175
Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
      180      185      190
Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
      195      200      205
Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

```

210	215	220
Ser Gly Asp Leu Ser	Lys Ala Phe Val Ser	Cys Ser Asp His Ile Thr
225	230	235
Val Gly Ile Leu Phe	Phe Met Pro Cys Ile	Phe Leu Tyr Val Xaa Pro
245	250	255
Leu Pro Lys Thr Thr	His Asp Xaa Tyr Leu	Phe Ile Val Pro Leu Leu
260	265	270
Ser Pro Leu Ser Arg	Ile Tyr Thr Leu Arg	Asn Lys Asp Met Asn Val
275	280	285
Ser Met Glu Arg Leu	Gly Lys Trp Ile Ala	Gly Ser Ser Arg Met Ser
290	295	300
Xaa Xaa Met Val Leu	Ser Arg Val Gln Asp	Asp Ser Val Ser Pro
305	310	315

&lt;210&gt; 1271

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g188 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1271

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg	1	5	10	15
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe	20	25	30	
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu	35	40	45	
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met	50	55	60	
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr	65	70	75	80
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser	85	90	95	
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe	100	105	110	
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr	115	120	125	
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln	130	135	140	
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr	145	150	155	160
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met	165	170	175	
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val	180	185	190	
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala	195	200	205	
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala	210	215	220	
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln	225	230	235	240
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe	245	250	255	
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala	260	265	270	
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro	275	280	285	
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala	290	295	300	

Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn  
 305 310 315 320  
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile  
 130 135 140  
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu  
 145 150 155 160  
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys  
 165 170 175  
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala  
 180 185 190  
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile  
 195 200 205  
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu  
 210 215 220  
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser  
 225 230 235 240  
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val  
 245 250 255  
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser  
 260 265 270  
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr  
 275 280 285  
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 290 295 300  
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro  
 305 310 315 320  
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1          5          10          15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
          20          25          30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
          35          40          45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
          85          90          95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
          100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
          115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
          130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
          165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
          180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
          195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
          210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
          245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
          260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
          290          295          300
Gln Arg Arg Gln Asp Ser Arg
305          310

```

&lt;210&gt; 1274

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g191 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1          5          10          15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
          20          25          30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
          35          40          45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
 50 55 60  
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
 65 70 75 80  
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
 85 90 95  
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
 100 105 110  
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
 115 120 125  
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Ile  
 130 135 140  
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu  
 145 150 155 160  
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
 165 170 175  
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
 180 185 190  
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300

Phe  
 305

<210> 1275

<211> 312

<212> PRT

<213> Unknown (H38g192 protein)

<220>

<223> Synthetic construct

<400> 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu  
 20 25 30  
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr  
 35 40 45  
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser  
 100 105 110  
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

130	135	140
Val Ala Ala Ala Cys	Ala Cys Gly Phe Thr	Val Ala Gln Ile Ile Thr
145	150	155
Ser Leu Val Phe His	Leu Pro Phe Tyr Ser	Ser Asn Gln Leu His His
165	170	175
Phe Phe Cys Asp Ile	Ala Pro Val Leu Lys	Leu Ala Ser His His Asn
180	185	190
His Phe Ser Gln Ile	Val Ile Phe Met Leu Cys	Thr Leu Val Leu Ala
195	200	205
Ile Pro Leu Leu Leu	Ile Leu Val Ser Tyr	Val His Ile Leu Ser Ala
210	215	220
Ile Leu Gln Phe Pro	Ser Thr Leu Gly Arg	Cys Lys Ala Phe Ser Thr
225	230	235
Cys Val Ser His Leu	Ile Ile Val Thr Val	His Tyr Gly Cys Ala Ser
245	250	255
Phe Ile Tyr Leu Arg	Pro Gln Ser Asn Tyr	Ser Ser Ser Gln Asp Ala
260	265	270
Leu Ile Ser Val Ser	Tyr Thr Ile Ile Thr	Pro Leu Phe Asn Pro Met
275	280	285
Ile Tyr Ser Leu Arg	Asn Lys Glu Phe Lys	Ser Ala Leu Cys Lys Ile
290	295	300
Val Arg Arg Thr Ile	Ser Leu Leu	
305	310	

&lt;210&gt; 1276

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g193 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(244)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1276

Met Met Ile Ser Ser	Asp Glu Glu Asn Asp	Thr Asn Met Met Glu Phe
1	5	10
Ile Leu Val Gly Leu	Ser Arg Gln Pro Ala	Ser Gln Leu Leu Phe Phe
20	25	30
Xaa Ala Ile Leu Phe	Ile Tyr Ser Val Thr	Leu Val Gly Asn Ile Leu
35	40	45
Ile Ile Val Ile Ile	Gln Ile Asp Ser His	Leu Gln Thr Pro Met Tyr
50	55	60
Phe Phe Leu Ile Gln	Val Ser Phe Leu Asp	Ile Cys Ser Thr Pro Thr
65	70	75
Val Leu Val Asn Cys	Xaa Lys Asp Phe Pro	Ser Val Ser Tyr Ser Gly
85	90	95
Cys Leu Phe Xaa Met	Thr Ile Phe Leu Tyr	Leu Gly Val Thr Glu Cys
100	105	110
Val Phe Phe Leu Phe	Cys Phe Glu Cys Phe	Leu Ile Ala Val Met Ala
115	120	125
Tyr Asp Arg Phe Val	Ala Ile Ser Lys Pro	Leu Cys Tyr Pro Phe Ile
130	135	140
Ile Asn Ser Asn Val	Cys Ile Trp Met Val	Ala Gly Val Trp Ala His
145	150	155
Pro Gly Arg Thr Asn	Pro Ile Leu Trp Pro	Gln Cys Ser Gln His Phe
165	170	175
Thr Cys Glu Leu Gln	Val Ile Phe Lys Leu	Thr Cys Ser Pro Val Leu
180	185	190

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala  
 195 200 205  
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr  
 210 215 220  
 His Pro Arg Ser Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile  
 225 230 235 240  
 Ile Gly Val His

<210> 1277

<211> 306

<212> PRT

<213> Unknown (H38g194 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(306)

<223> Xaa = Any Amino Acid

<400> 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly  
 1 5 10 15  
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu  
 20 25 30  
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu  
 35 40 45  
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys  
 65 70 75 80  
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn  
 115 120 125  
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val  
 130 135 140  
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val  
 145 150 155 160  
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp  
 165 170 175  
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu  
 180 185 190  
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu  
 195 200 205  
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn  
 210 215 220  
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His  
 225 230 235 240  
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu  
 245 250 255  
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val  
 260 265 270  
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu  
 275 280 285  
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys  
 290 295 300  
 Leu Phe

305

&lt;210&gt; 1278

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g195 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1278

```

Met Ala Asn Ser Ser Ser Val Thr Glu Phe Leu Val Leu Gly Phe Ser
 1           5           10           15
Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe Leu Cys Leu
      20           25           30
Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ser Val Ile His
      35           40           45
Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu
      50           55           60
Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro Lys Met Leu
      65           70           75           80
Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val Ser Cys Ala
      85           90           95
Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn Cys Leu Leu
      100          105          110
Leu Gly Val Met Gly Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
      115          120          125
Gln Tyr Ala Val Leu Met Ser Trp Arg Val Cys Gly Gln Leu Ile Ala
      130          135          140
Thr Cys Ile Ile Ser Gly Phe Leu Ile Ser Leu Val Gly Thr Thr Phe
      145          150          155          160
Val Phe Ser Leu Pro Phe Cys Gly Ser Asn Lys Val Asn His Tyr Phe
      165          170          175
Cys Asp Ile Ser Pro Val Ile Arg Leu Ala Cys Ala Asp Ser Tyr Ile
      180          185          190
Ser Glu Leu Val Ile Phe Ile Phe Gly Val Leu Val Leu Val Val Pro
      195          200          205
Leu Ile Phe Ile Cys Ile Ser Tyr Gly Phe Ile Val Arg Thr Ile Leu
      210          215          220
Lys Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
      225          230          235          240
Ser His Leu Ile Val Val Ile Val His Tyr Gly
      245          250

```

&lt;210&gt; 1279

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g196 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1279

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1           5           10           15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
      20           25           30

```



Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile  
 35 40 45  
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe  
 50 55 60  
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser  
 65 70 75 80  
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile  
 85 90 95  
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly  
 100 105 110  
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val  
 115 120 125  
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val  
 130 135 140  
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala  
 145 150 155 160  
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val  
 165 170 175  
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys  
 180 185 190  
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe  
 195 200 205  
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile  
 210 215 220  
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met  
 245 250 255  
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val  
 260 265 270  
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr  
 275 280 285  
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys  
 290 295 300  
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn  
 305 310 315

&lt;210&gt; 1280

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g197 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro  
 20 25 30  
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn  
 35 40 45  
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser  
 65 70 75 80  
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn  
 85 90 95  
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile  
 100 105 110  
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

```

      115      120      125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
  130      135      140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
  145      150      155      160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
      165      170      175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
      180      185      190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
      195      200      205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
  210      215      220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
  225      230      235      240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
      245      250      255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
      260      265      270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
      275      280      285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
  290      295      300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
  305      310      315

```

&lt;210&gt; 1281

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g198 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1281

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1      5      10      15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
      20      25      30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
      35      40      45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
      50      55      60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
      65      70      75      80
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
      85      90      95
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
      100      105      110
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
      115      120      125
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
      130      135      140
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
      145      150      155

```

&lt;210&gt; 1282

<211> 317  
 <212> PRT  
 <213> Unknown (H38g199 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1282  
 Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu  
 1 5 10 15  
 Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu  
 20 25 30  
 Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Ile Leu  
 35 40 45  
 Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg  
 50 55 60  
 Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys  
 65 70 75 80  
 Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala  
 85 90 95  
 Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu  
 100 105 110  
 Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser  
 115 120 125  
 Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val  
 130 135 140  
 Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile  
 145 150 155 160  
 Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe  
 165 170 175  
 Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa  
 180 185 190  
 Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe  
 195 200 205  
 Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val  
 210 215 220  
 Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr  
 225 230 235 240  
 Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe  
 245 250 255  
 Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys  
 260 265 270  
 Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu  
 275 280 285  
 Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser  
 290 295 300  
 Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val  
 305 310 315

<210> 1283  
 <211> 302  
 <212> PRT  
 <213> Unknown (H38g200 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1          5          10          15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
          20          25          30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Leu Gly Asn Gly Thr Ile Leu
          35          40          45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
          50          55          60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
          65          70          75          80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
          85          90          95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
          100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
          130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
          145          150          155          160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
          165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
          180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
          195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
          210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
          225          230          235          240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
          245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
          260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300

```

&lt;210&gt; 1284

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g201 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20          25          30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35          40          45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
          50          55          60

```

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100         105         110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115         120         125
Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130         135         140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145         150         155         160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165         170         175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
          180         185         190
Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
          195         200         205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
          210         215         220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
          225         230         235         240
Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
          245         250         255
Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
          260         265         270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275         280         285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290         295         300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
          305         310         315         320
Phe Phe Trp Cys

```

&lt;210&gt; 1285

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g202 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(144)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1285

```

Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
1          5          10          15
Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
          20          25          30
Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu
          35          40          45
Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
          50          55          60
Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
          65          70          75          80
Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
          85          90          95
Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

```

	100		105		110										
Asp	Leu	Ala	Leu	Lys	Gln	Asn	Phe	Ala	Ile	Leu	Arg	Ser	Ile	Pro	Ser
	115		120		125										
Phe	Ser	Ser	Xaa	Asp	Leu	Glu	Ile	His	Asn	Val	Arg	Tyr	Gln	His	Phe
	130				135						140				

&lt;210&gt; 1286

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g203 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1286

Thr	His	Gly	Tyr	Thr	Phe	Ser	Leu	Arg	Leu	Phe	Leu	His	Cys	Leu	Thr
1				5					10					15	
Tyr	Val	Xaa	Val	Ser	His	Cys	Leu	Leu	Ile	Trp	Leu	Ile	Thr	Phe	Ser
			20					25					30		
Pro	Phe	Asn	Leu	Leu	Phe	Lys	Xaa	Asn	Leu	Xaa	Phe	Thr	Ile	Xaa	Leu
		35					40					45			
Ile	Thr	Xaa	Ile	Glu	Ser	Arg	Tyr	Ser	Lys	His	Trp	Pro	Phe	Phe	Leu
	50					55					60				
Leu	Xaa	Cys	Phe	Cys	Asn	Val	Leu	Phe	His	Leu	Asp	Cys	Asp	Ser	Pro
65					70					75				80	
Val	Cys	Asn	Thr	Lys	Arg	Ile	Arg	Ser	Phe	Phe	Val	Leu	Glu	Arg	Xaa
				85					90					95	
Lys	Ser	Ser	Xaa	Lys	Ser	Glu	Lys	Ile	His	Phe	Xaa	Thr	Arg	Asn	Lys
			100					105					110		
Val	Ser	Cys	Phe	Xaa	Asp	Phe	Gly	Ile	Lys	Tyr	Thr	Val	Tyr	Leu	Leu
	115						120					125			
Leu	Leu	Lys	His	Phe	Leu	Leu	Ile	His	Ser	Ile	Leu	Arg	Tyr	Leu	Xaa
	130					135					140				
Val	Ala	Gly	Tyr	Gly	Thr	Ser	Xaa	Phe	Leu	Ser	Arg	Ile	Ser	Ser	Ile
145					150					155					160
Thr	Leu	Lys	Thr	Ile	Ile	Cys	Ile	Leu	Lys	Lys	Ser	Tyr	His	Phe	Phe
				165					170					175	
Ser	Val	Gln	Tyr	Thr	Ile	Ser	Tyr	Ile	Asp	Pro	Phe	Ile	Asn	Ser	Leu
		180						185					190		
Val	Met	Phe	Val	Val	Phe	Thr	Ala	Phe	Ile	Gln	Ala	Phe	Ala	Phe	Met
	195						200					205			
Ile	Ile	Ile	Val	Ser	Tyr	Thr	Gln	Val	Leu	Phe	Ala	Leu	Leu	Lys	Lys
	210					215					220				
Asn	Ser	Glu	Lys	Gly	Arg	Ser	Lys	Ser	Phe	Leu	Met	Cys	Ser	Ala	His
225					230					235				240	
Leu	Leu	Ser	Val	Ser	Leu	Phe	Tyr	Ser	Ser	Val	Phe	Phe	Met	Tyr	Gly
				245					250					255	
Cys	Pro	Arg	Ser	Gly	Pro	Asp	Xaa	Gln	Trp	Asn	Glu	Met	Tyr	Phe	Pro
			260					265					270		
Phe	Tyr	Met	Ile	Ile	Ile	Pro	Leu	Gln	Thr	Pro	Phe	Ile	Tyr	Ser	Met
	275						280					285			
Lys	Asn	Lys	Glu	Val	Leu	Gly	Thr	Leu	Arg	Thr	Met	Ile	Lys	Lys	Tyr
	290					295					300				
Phe	Trp	Arg	Thr	Leu	Ser	Xaa	Phe	Phe	Pro						
305					310										

&lt;210&gt; 1287

<211> 253  
 <212> PRT  
 <213> Unknown (H38g204 protein)

<220>  
 <223> Synthetic construct

<400> 1287

```

Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser
 1           5           10           15
Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg
      20           25           30
Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe
 35           40           45
Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg
 50           55           60
Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His
 65           70           75           80
Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile
      85           90           95
His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly
      100           105           110
Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg
      115           120           125
Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp
      130           135           140
Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr
      145           150           155           160
Gly Tyr Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg
      165           170           175
Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val
      180           185           190
Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu
      195           200           205
Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu
      210           215           220
Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala
      225           230           235           240
Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His
      245           250

```

<210> 1288  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g205 protein)

<220>  
 <223> Synthetic construct

<400> 1288

```

Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1           5           10           15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
      20           25           30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
      35           40           45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
      65           70           75           80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

```

<210> 1289  
<211> 311  
<212> PRT  
<213> Unknown (H38g206 protein)

<220>  
<223> Synthetic construct

<400> 1289																
Met	Lys	Ile	Lys	Asn	His	Thr	Pro	Val	Thr	Glu	Val	Pro	Leu	Met	Gly	
1				5					10					15		
Ile	Pro	His	Thr	Lys	Gly	Met	Glu	Asn	Val	Leu	Phe	Val	Leu	Phe	Leu	
			20					25					30			
Ala	Phe	Tyr	Leu	Phe	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala	
		35					40					45				
Val	Leu	Thr	Phe	Ser	Asn	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	
	50					55					60					
Asn	Leu	Ser	Val	Phe	Asp	Ile	Phe	Phe	Pro	Ser	Val	Ser	Ser	Pro	Lys	
65					70					75					80	
Met	Met	Leu	Cys	Leu	Val	Gly	Gln	Ser	Cys	Thr	Ile	Ser	Phe	Gln	Gly	
				85					90					95		
Cys	Ala	Ser	Gln	Leu	Phe	Phe	His	His	Phe	Leu	Gly	Cys	Thr	Glu	Cys	
			100					105					110			
Phe	Leu	Tyr	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Ala	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	Pro	Tyr	Thr	Val	Ile	Met	Lys	Arg	Arg	Val	Cys	Ala	Leu	Leu	
		130				135					140					
Thr	Leu	Gly	Thr	Trp	Thr	Gly	Ser	Cys	Leu	His	Ala	Ser	Val	Leu	Thr	
145					150					155					160	
Leu	Leu	Ile	Phe	Lys	Leu	Ser	Tyr	Cys	Gly	Pro	Asn	Glu	Val	Asp	Asn	
				165					170					175		



Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr  
 180 185 190  
 Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu  
 195 200 205  
 Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser  
 210 215 220  
 Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val  
 245 250 255  
 Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val  
 260 265 270  
 Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile  
 290 295 300  
 Gln Gly Val His Asn Cys Gly  
 305 310

&lt;210&gt; 1290

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g207 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(298)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1290

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe  
 1 5 10 15  
 Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe  
 20 25 30  
 Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Val Gly Ser His Met  
 35 40 45  
 Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln  
 65 70 75 80  
 Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala  
 85 90 95  
 Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser  
 100 105 110  
 Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln  
 115 120 125  
 Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu  
 130 135 140  
 Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser  
 145 150 155 160  
 Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr  
 180 185 190  
 Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala  
 195 200 205  
 His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val  
 210 215 220  
 Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

225		230		235		240
Ala His Leu Ala Met Ile Gly Leu Phe Tyr Val Thr Ser Val Pro Cys						
	245		250		255	
Tyr Ile Leu Pro Asn Ser Ala Tyr Ser Gly Leu Gly Asp Trp Val Leu						
	260		265		270	
Ser Val Leu Cys Val Val Leu Thr His Met Leu Asn Pro Ile Phe Pro						
	275		280		285	
Ser Met Leu Gly Xaa Gln Cys Met Ser His						
	290		295			

&lt;210&gt; 1291

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g208 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1291

Met Gly Val Lys Asn His Ser Thr Val Thr Glu Phe Leu Leu Ser Gly															
1		5		10		15									
Leu Thr Glu Gln Ala Glu Leu Gln Leu Pro Leu Phe Cys Leu Phe Leu															
	20		25		30										
Gly Ile Tyr Thr Val Thr Val Val Gly Asn Leu Ser Met Ile Ser Ile															
	35		40		45										
Ile Arg Leu Asn Arg Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser															
	50		55		60										
Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys															
	65		70		75										
Met Leu Ser Gly Phe Leu Cys Arg Asp Arg Ser Ile Ser Tyr Ser Gly															
	85		90		95										
Cys Met Ile Gln Leu Phe Phe Phe Cys Val Cys Val Ile Ser Glu Cys															
	100		105		110										
Tyr Met Leu Ala Ala Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Ser															
	115		120		125										
Pro Leu Leu Tyr Arg Val Ile Met Ser Pro Arg Val Cys Ser Leu Leu															
	130		135		140										
Val Ala Ala Val Phe Ser Val Gly Phe Thr Asp Ala Val Ile His Gly															
	145		150		155										
Gly Cys Ile Leu Arg Leu Ser Phe Cys Gly Ser Asn Ile Ile Lys His															
	165		170		175										
Tyr Phe Cys Asp Ile Val Pro Leu Ile Lys Leu Ser Cys Ser Ser Thr															
	180		185		190										
Tyr Ile Asp Glu Leu Leu Ile Phe Val Ile Gly Gly Phe Asn Met Val															
	195		200		205										
Ala Thr Ser Leu Thr Ile Ile Ser Tyr Ala Phe Ile Leu Thr Ser															
	210		215		220										
Ile Leu Arg Ile His Ser Lys Lys Gly Arg Cys Lys Ala Phe Ser Thr															
	225		230		235										
Cys Ser Ser His Leu Thr Ala Val Leu Met Phe Tyr Gly Ser Leu Met															
	245		250		255										
Ser Met Tyr Leu Lys Pro Ala Ser Ser Ser Leu Thr Gln Glu Lys															
	260		265		270										
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Leu Met Leu Asn Pro Leu															
	275		280		285										
Ile Tyr Ser Leu Arg Asn Asn Glu Val Arg Asn Ala Leu Met Lys Leu															
	290		295		300										
Leu Arg Arg Lys Ile Ser Leu Ser															
	305		310												

&lt;210&gt; 1292

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g209 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1292

```

Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1          5          10          15
Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
          20          25          30
Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
          35          40          45
Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
          50          55          60
Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
65          70          75          80
Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
          85          90          95
Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
          100          105          110
Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
          115          120          125
Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
          130          135          140
Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
145          150          155          160
Ile Phe Ile Ile Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
          165          170          175
His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
          180          185          190
Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
          195          200          205
Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
210          215          220
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
225          230          235          240
Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
          245          250

```

&lt;210&gt; 1293

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g210 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1293

```

Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1          5          10          15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
65          70          75          80
Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys

```

				85					90					95			
Val	Ala	Gln	Leu	Tyr	Phe	Phe	His	Phe	Leu	Gly	Ser	Thr	Glu	Cys	Phe		
			100					105					110				
Leu	Tyr	Thr	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Leu	Ala	Ile	Ser	Tyr	Pro		
		115					120					125					
Leu	Arg	Tyr	Thr	Asn	Met	Met	Thr	Gly	Arg	Ser	Cys	Ala	Leu	Leu	Ala		
	130					135					140						
Thr	Gly	Thr	Trp	Leu	Ser	Gly	Ser	Leu	His	Ser	Ala	Val	Gln	Thr	Ile		
145					150					155					160		
Leu	Thr	Phe	His	Leu	Pro	Tyr	Cys	Gly	Pro	Asn	Gln	Ile	Gln	His	Tyr		
			165					170						175			
Phe	Cys	Asp	Ala	Pro	Pro	Ile	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	Ser		
		180						185					190				
Ala	Asn	Glu	Met	Val	Ile	Phe	Val	Asn	Ile	Gly	Leu	Val	Ala	Ser	Gly		
	195						200					205					
Cys	Phe	Val	Leu	Ile	Val	Leu	Ser	Tyr	Val	Ser	Ile	Val	Cys	Ser	Ile		
	210					215					220						
Leu	Arg	Ile	Arg	Thr	Ser	Glu	Gly	Arg	His	Arg	Ala	Phe	Gln	Thr	Cys		
225					230					235					240		
Ala	Ser	His	Cys	Ile	Val	Val	Leu	Cys	Phe	Phe	Gly	Pro	Gly	Leu	Phe		
			245					250					255				
Ile	Tyr	Leu	Arg	Pro	Gly	Ser	Arg	Asp	Ala	Leu	His	Gly	Val	Val	Ala		
		260						265					270				
Val	Phe	Tyr	Thr	Thr	Leu	Thr	Pro	Leu	Phe	Asn	Pro	Val	Val	Tyr	Thr		
		275					280					285					
Leu	Arg	Asn	Lys	Glu	Val	Lys	Lys	Ala	Leu	Leu	Lys	Leu	Lys	Asn	Gly		
	290					295					300						
Ser	Val	Phe	Ala	Gln	Gly	Glu											
305					310												

&lt;210&gt; 1294

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g211 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(278)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1294

His	Ser	Ser	Leu	Leu	Phe	Ala	Val	Phe	Leu	Leu	Thr	Tyr	Ser	Val	Thr		
1				5				10						15			
Leu	Val	Gly	Asn	Leu	Gly	Met	Thr	Asp	Leu	Ile	Cys	Gln	Ser	Arg	Thr		
		20						25				30					
Ser	Ser	Ala	Leu	His	Thr	Pro	Met	Cys	Phe	Leu	Leu	Ser	Val	Phe	Ser		
		35				40						45					
Phe	Leu	Asp	Ile	Cys	Ser	Ser	Ser	Ile	Val	His	Pro	Arg	Leu	Leu	Ile		
	50				55					60							
His	Phe	Leu	Thr	Thr	Arg	Pro	Ser	Ile	Ser	Phe	Ala	Gly	Gly	Ile	Ile		
65					70					75				80			
Gln	Met	Ala	Leu	Met	Thr	Phe	Tyr	Gly	Thr	Gly	Glu	Cys	Leu	Leu	Leu		
			85					90					95				
Ala	Ile	Val	Ala	Tyr	Asp	Xaa	Val	Val	Ala	Ile	Cys	His	Pro	Phe	Pro		
		100						105					110				
Xaa	His	Ile	Ile	Met	Ser	Lys	Gly	Leu	Cys	Ala	Gln	Leu	Val	Val	Val		
	115					120					125						
Thr	Ser	Ala	Val	Gly	Val	Leu	Ile	Ser	Ala	His	Arg	Gln	Asp	Ala	Phe		
	130					135					140						

```

Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser
145          150          155          160
Val Thr Phe Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr
          165          170          175
Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro
          180          185          190
Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu
          195          200          205
Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg
          210          215          220
Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu
225          230          235          240
Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile
          245          250          255
Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu
          260          265          270
Arg Asn Lys Asp Val Lys
          275

```

&lt;210&gt; 1295

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g212 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1295

```

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu
1      5      10      15
Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe
20     25     30
Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met
35     40     45
Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu
50     55     60
Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro
65     70     75     80
Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr
85     90     95
Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu
100    105    110
Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
115    120    125
Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu
130    135    140
Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr
145    150    155    160
Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His
165    170    175
Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr
180    185    190
His Val Lys Glu Leu Met Leu Leu Ile Ile Ala Gly Phe Asn Thr Leu
195    200    205
Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala
210    215    220
Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225    230    235    240
Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile
245    250    255
Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

```

260 265 270  
 Val Ala Ser Val Phe Asn Val Val Val Ile Pro Thr Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Leu Lys Arg Ile  
 290 295 300  
 Ile Glu Lys Leu Cys Leu Ala Val  
 305 310

<210> 1296  
 <211> 232  
 <212> PRT  
 <213> Unknown (H38g213 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(232)  
 <223> Xaa = Any Amino Acid

<400> 1296  
 Ser Gly Leu Val Pro Lys Ser Phe Pro Gly Cys Leu Thr Gln Leu Phe  
 1 5 10 15  
 Phe Leu His Tyr Ser Phe Val Leu Asp Ser Ala Ile Leu Leu Ala Met  
 20 25 30  
 Ala Phe Asp Arg Tyr Met Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr  
 35 40 45  
 Ile Leu Thr Pro Lys Thr Ile Val Lys Ile Ala Val Gly Ile Cys Phe  
 50 55 60  
 Arg Ser Phe Cys Val Phe Val Pro Cys Val Phe Leu Val Asn Arg Leu  
 65 70 75 80  
 Pro Phe Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys Glu His Ile  
 85 90 95  
 Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Ile Trp Cys  
 100 105 110  
 Gly Phe Cys Val Pro Ile Met Thr Val Met Thr Asp Val Ile Leu Ile  
 115 120 125  
 Ala Val Ser Tyr Thr Leu Ile Leu Cys Ala Val Phe Cys Leu Pro Ser  
 130 135 140  
 Gln Asp Ala Arg Gln Lys Ala Leu Cys Ser Cys Gly Ser His Val Cys  
 145 150 155 160  
 Val Ile Leu Ile Phe Tyr Ile Pro Ala Phe Phe Ser Ile Leu Ala His  
 165 170 175  
 Cys Phe Gly His Asn Val Pro His Thr Phe His Ile Met Phe Ala Asn  
 180 185 190  
 Leu Tyr Val Ile Ile Pro Pro Ala Leu Asn Ser Ile Val Tyr Arg Ile  
 195 200 205  
 Lys Thr Lys Gln Ile Gln Asn Arg Ile Leu Leu Leu Phe Pro Lys Gly  
 210 215 220  
 Ser Gln Xaa Xaa Val Pro Glu Leu  
 225 230

<210> 1297  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g214 protein)

<220>  
 <223> Synthetic construct

<400> 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
1      5      10      15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
20      25      30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
35      40      45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
50      55      60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
65      70      75      80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
85      90      95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
100     105     110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
115     120     125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
130     135     140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
145     150     155     160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
165     170     175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
180     185     190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
195     200     205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
210     215     220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
225     230     235     240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
245     250     255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
260     265     270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
275     280     285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
290     295     300
Val Ala His Ser Gln Ser
305     310

```

&lt;210&gt; 1298

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g215 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
1      5      10      15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
20      25      30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
35      40      45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
50      55      60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
65      70      75      80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

				85					90					95					
Leu	Val	Gln	Cys	Tyr	Leu	Phe	Ile	Ala	Leu	Val	His	Val	Glu	Ile	Tyr				
			100					105					110						
Ile	Leu	Ala	Val	Met	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro				
		115					120					125							
Leu	Leu	Tyr	Gly	Ser	Arg	Met	Ser	Lys	Ser	Val	Cys	Ser	Phe	Leu	Ile				
	130					135					140								
Thr	Val	Pro	Tyr	Val	Tyr	Gly	Ala	Leu	Thr	Gly	Leu	Met	Glu	Thr	Met				
145					150					155					160				
Trp	Thr	Tyr	Asn	Leu	Ala	Phe	Cys	Gly	Pro	Asn	Glu	Ile	Asn	His	Phe				
			165					170					175						
Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr				
		180					185						190						
Asn	Lys	Glu	Leu	Ser	Met	Phe	Ile	Val	Ala	Gly	Trp	Asn	Leu	Ser	Phe				
	195					200						205							
Ser	Leu	Phe	Ile	Ile	Cys	Ile	Ser	Tyr	Leu	Tyr	Ile	Phe	Pro	Ala	Ile				
	210				215						220								
Leu	Lys	Ile	Arg	Ser	Thr	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys				
225					230				235						240				
Gly	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Ala	Thr	Leu	Phe	Phe				
				245				250					255						
Met	Tyr	Leu	Arg	Pro	Pro	Ser	Lys	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met				
		260					265						270						
Val	Ala	Val	Phe	Tyr	Thr	Thr	Val	Ile	Pro	Met	Leu	Asn	Leu	Ile	Ile				
		275				280						285							
Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys	Glu	Ala	Leu	Ile	Lys	Glu	Leu				
	290				295						300								
Ser	Met	Lys	Ile	Tyr	Phe	Ser													
305					310														

&lt;210&gt; 1299

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g216 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1299

Met	Leu	Leu	Ser	Asn	Ile	Thr	Gln	Phe	Ser	Pro	Ile	Phe	Tyr	Leu	Thr				
1				5				10					15						
Ser	Phe	Pro	Gly	Leu	Glu	Gly	Ile	Lys	His	Trp	Ile	Phe	Ile	Pro	Phe				
		20					25					30							
Phe	Phe	Met	Tyr	Met	Val	Ala	Ile	Ser	Gly	Asn	Cys	Phe	Ile	Leu	Ile				
		35					40					45							
Ile	Ile	Lys	Thr	Asn	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Tyr	Leu	Leu				
	50					55				60									
Ser	Leu	Leu	Ala	Leu	Thr	Asp	Leu	Gly	Leu	Cys	Val	Ser	Thr	Leu	Pro				
65					70				75					80					
Thr	Thr	Met	Gly	Ile	Phe	Trp	Phe	Asn	Ser	Gln	Ser	Ile	Tyr	Phe	Gly				
			85					90					95						
Ala	Cys	Gln	Ile	Gln	Met	Phe	Cys	Ile	His	Ser	Phe	Ser	Phe	Met	Glu				
		100					105						110						
Ser	Ser	Val	Leu	Leu	Met	Met	Ser	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys				
		115					120					125							
His	Pro	Leu	Arg	Tyr	Ser	Val	Ile	Ile	Thr	Gly	Gln	Gln	Val	Val	Arg				
	130					135					140								
Ala	Gly	Leu	Ile	Val	Ile	Phe	Arg	Gly	Pro	Val	Ala	Thr	Ile	Pro	Ile				
145					150					155					160				
Val	Leu	Leu	Leu	Lys	Ala	Phe	Pro	Tyr	Cys	Gly	Ser	Val	Val	Leu	Ser				
			165					170						175					



His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp  
 180 185 190  
 Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val  
 195 200 205  
 Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His  
 210 215 220  
 Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln  
 225 230 235 240  
 Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met  
 245 250 255  
 Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala  
 260 265 270  
 Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile  
 290 295 300  
 Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys  
 305 310 315

&lt;210&gt; 1300

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g217 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1300

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly  
 1 5 10 15  
 Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met  
 20 25 30  
 Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg  
 50 55 60  
 Asn Phe Ser Phe Leu Glu Leu Leu Val Thr Val Val Val Pro Lys  
 65 70 75 80  
 Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser  
 85 90 95  
 Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe  
 100 105 110  
 Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu  
 130 135 140  
 Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr  
 145 150 155 160  
 Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His  
 165 170 175  
 Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr  
 180 185 190  
 His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu  
 195 200 205  
 Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr  
 210 215 220  
 Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile  
 245 250 255  
 Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

260 265 270  
 Gly Ala Ser Val Leu Ser Cys Ile Ile Thr Pro Leu Leu Asn Pro Phe  
 275 280 285  
 Ile Phe Thr Leu Arg Asn Asp Lys Val Gln Gln Ala Leu Arg Glu Ala  
 290 295 300  
 Leu Gly Trp Pro Arg Leu Thr Ala Val Met Lys Leu Arg Val Thr Ser  
 305 310 315 320  
 Gln Arg Lys

<210> 1301

<211> 338

<212> PRT

<213> Unknown (H38g218 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1301

Met Met Gly Glu Ala Arg Asn Arg Thr Val Val Gln Glu Phe Ile Leu  
 1 5 10 15  
 Glu Gly Phe Pro Ala Val Gln His Leu Gly Asn Val Leu Phe Leu Val  
 20 25 30  
 His Leu Leu Ala Tyr Leu Ala Ser Ile Met Ala Asn Met Leu Ile Ile  
 35 40 45  
 Thr Ile Thr Trp Ala Asp His His Leu Gln Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Asn Ser Phe Ser Phe Cys Glu Cys Cys Phe Ile Thr Thr Val Ile  
 65 70 75 80  
 Pro Lys Leu Leu Val Ile Phe Leu Ser Gly Arg Gln Ile Ile Pro Phe  
 85 90 95  
 Thr Thr Cys Leu Met Gln Ser Phe Ser Phe Leu Phe Leu Gly Ser Thr  
 100 105 110  
 Val Phe Phe Leu Met Ala Val Met Ser Leu Asp Xaa Tyr Leu Ala Ile  
 115 120 125  
 Cys Lys Pro Leu His Tyr Ser Thr Ile Met Ser Leu Arg Thr Ser Phe  
 130 135 140  
 His Leu Val Thr Val Cys Phe Val Val Gly Phe Thr Leu Ile Thr Gly  
 145 150 155 160  
 Leu Met Val Lys Val Ser Gln Leu Ser Phe Cys Gly Pro His Val Ile  
 165 170 175  
 Pro His Phe Phe Arg Asp Leu Gly Pro Leu Ile Gln Leu Ser Cys Ser  
 180 185 190  
 Asp Thr Arg Ser Thr Glu Thr Leu Ala Phe Val Leu Val Ser Phe Val  
 195 200 205  
 Leu Phe Thr Ser Leu Ile Ile Thr Ile Ile Ala Tyr Gly Asn Ile Val  
 210 215 220  
 Val Thr Ile Val Arg Leu Pro Ser Ala Lys Glu Arg Gln Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Ser Ser His Leu Ile Val Leu Ser Leu Val Tyr Gly Ser  
 245 250 255  
 Cys Val Phe Ile Tyr Val Lys Pro Lys Gln Met Asp Arg Leu Asp Ser  
 260 265 270  
 Asn Arg Met Ala Ala Leu Val Asn Thr Val Val Thr Pro Leu Leu Asn  
 275 280 285  
 Pro Ile Ile Tyr Thr Leu Arg Asn Lys Gln Val His Gln Ala Leu Arg  
 290 295 300

Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln  
 305 310 315 320  
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe  
 325 330 335  
 Trp Asn

<210> 1302  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g219 protein)

<220>  
 <223> Synthetic construct

<400> 1302  
 Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe  
 1 5 10 15  
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val  
 20 25 30  
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser  
 35 40 45  
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu  
 50 55 60  
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile  
 65 70 75 80  
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu  
 85 90 95  
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu  
 100 105 110  
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala  
 130 135 140  
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val  
 145 150 155 160  
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe  
 165 170 175  
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met  
 180 185 190  
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser  
 195 200 205  
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg  
 210 215 220  
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser  
 225 230 235 240  
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr  
 245 250 255  
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu  
 290 295 300  
 Asn Pro Gly Arg Glu  
 305

<210> 1303  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g220 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
 20          25          30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
 35          40          45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65          70          75          80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
 85          90          95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
 100         105         110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115         120         125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
 130         135         140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
 145         150         155         160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
 165         170         175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
 180         185         190
Val Lys Glu Leu Met Leu Phe Ile Ala Ala Phe Asn Val Phe Cys
 195         200         205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
 210         215         220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225         230         235         240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
 245         250         255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
 260         265         270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
 275         280         285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
 290         295         300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
 305         310         315         320
Glu Ile

```

&lt;210&gt; 1304

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g221 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1          5          10          15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20          25          30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
          35          40          45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
 50          55          60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65          70          75          80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85          90          95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
          130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
          145          150          155          160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Leu Ile
          195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
          210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
          225          230          235          240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
          290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
          305          310          315

```

&lt;210&gt; 1305

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g222 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20          25          30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35          40          45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50          55          60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
          65          70          75          80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

```

				85					90				95				
Cys	Leu	Thr	Gln	Leu	Phe	Phe	Phe	His	Phe	Ile	Gly	Gly	Ile	Lys	Ile		
			100					105					110				
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Ser	Gln		
			115					120					125				
Pro	Leu	His	Tyr	Thr	Leu	Ile	Met	Asn	Gln	Thr	Val	Cys	Ala	Leu	Leu		
			130				135					140					
Met	Ala	Ala	Ser	Trp	Val	Gly	Gly	Phe	Ile	His	Ser	Ile	Val	Gln	Ile		
145					150					155					160		
Ala	Leu	Thr	Ile	Gln	Leu	Pro	Phe	Cys	Gly	Pro	Asp	Lys	Leu	Asp	Asn		
				165					170					175			
Phe	Tyr	Cys	Asp	Val	Pro	Gln	Leu	Ile	Lys	Leu	Ala	Cys	Thr	Asp	Thr		
			180					185					190				
Phe	Val	Leu	Glu	Leu	Leu	Met	Val	Ser	Asn	Asn	Gly	Leu	Val	Thr	Leu		
			195				200					205					
Met	Trp	Phe	Leu	Val	Leu	Leu	Gly	Ser	Tyr	Thr	Ala	Leu	Leu	Val	Met		
			210				215					220					
Leu	Arg	Ser	His	Ser	Arg	Glu	Gly	Arg	Ser	Lys	Ala	Leu	Ser	Thr	Cys		
225					230					235					240		
Ala	Ser	His	Ile	Ala	Val	Val	Thr	Leu	Ile	Phe	Val	Pro	Cys	Ile	Tyr		
				245						250				255			
Val	Tyr	Thr	Arg	Pro	Phe	Arg	Thr	Phe	Pro	Met	Asp	Lys	Ala	Val	Ser		
			260					265					270				
Val	Leu	Tyr	Thr	Ile	Val	Thr	Pro	Met	Leu	Asn	Pro	Ala	Ile	Tyr	Thr		
			275				280					285					
Leu	Arg	Asn	Lys	Glu	Val	Ile	Met	Ala	Met	Lys	Lys	Leu	Trp	Arg	Arg		
			290			295					300						
Lys	Lys	Asp	Pro	Ile	Gly	Pro	Leu	Glu	His	Arg							
305					310					315							

&lt;210&gt; 1306

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g223 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1306

Met	Ser	Phe	Leu	Asn	Gly	Thr	Ser	Leu	Thr	Pro	Ala	Ser	Phe	Ile	Leu		
1				5					10					15			
Asn	Gly	Ile	Pro	Gly	Leu	Glu	Asp	Val	His	Leu	Trp	Ile	Ser	Phe	Pro		
			20					25					30				
Leu	Cys	Thr	Met	Tyr	Ser	Ile	Ala	Ile	Thr	Gly	Asn	Phe	Gly	Leu	Met		
			35				40					45					
Tyr	Leu	Ile	Tyr	Cys	Asp	Glu	Ala	Leu	His	Arg	Pro	Met	Tyr	Val	Phe		
			50			55				60							
Leu	Ala	Leu	Leu	Ser	Phe	Thr	Asp	Val	Leu	Met	Cys	Thr	Ser	Thr	Leu		
65					70				75					80			
Pro	Asn	Thr	Leu	Phe	Ile	Leu	Trp	Phe	Asn	Leu	Lys	Glu	Ile	Asp	Phe		
				85					90					95			
Lys	Ala	Cys	Leu	Ala	Gln	Met	Phe	Phe	Val	His	Thr	Phe	Thr	Gly	Met		
			100					105					110				
Glu	Ser	Gly	Val	Leu	Met	Leu	Met	Ala	Leu	Asp	His	Cys	Val	Ala	Ile		
			115				120					125					
Cys	Phe	Pro	Leu	Arg	Tyr	Ala	Thr	Ile	Leu	Thr	Asn	Ser	Val	Ile	Ala		
			130			135					140						
Lys	Ala	Gly	Phe	Leu	Thr	Phe	Leu	Arg	Gly	Val	Met	Leu	Val	Ile	Pro		
145					150					155					160		
Ser	Thr	Phe	Leu	Thr	Lys	Arg	Leu	Pro	Tyr	Cys	Lys	Gly	Asn	Val	Ile		
				165					170					175			

```

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
      180      185      190
Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
      195      200      205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
      210      215      220
Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
      225      230      235      240
Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
      245      250      255
Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro
      260      265      270
Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro
      275      280      285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu
      290      295      300
Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe
      305      310      315      320

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&lt;210&gt; 1307

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g224 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1307

```

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
  1      5      10      15
Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
      20      25      30
Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
      35      40      45
Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
      50      55      60
Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
      65      70      75      80
Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
      85      90      95
Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
      100      105      110
Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
      130      135      140
Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
      145      150      155      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
      165      170      175
Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
      180      185      190
Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
      195      200      205
Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
      210      215      220
Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser
      225      230      235      240
His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
      245      250      255
Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

```

260 265 270  
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg  
 275 280 285  
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val  
 290 295 300  
 Ile  
 305

<210> 1308

<211> 313

<212> PRT

<213> Unknown (H38g225 protein)

<220>

<223> Synthetic construct

<400> 1308

Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly  
 1 5 10 15  
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu  
 20 25 30  
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu  
 35 40 45  
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln  
 50 55 60  
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu  
 85 90 95  
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val  
 100 105 110  
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu  
 130 135 140  
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser  
 145 150 155 160  
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val  
 195 200 205  
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser  
 210 215 220  
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu  
 245 250 255  
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp  
 260 265 270  
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg  
 290 295 300  
 Phe Met Thr Asn Leu Cys Tyr Ser Phe  
 305 310

<210> 1309

<211> 326

<212> PRT



<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

```

Met Lys Ile Ser Asn Asn Ser Leu Gly Phe Leu Pro Thr Thr Phe Ile
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Ser Glu His Leu Trp Ile Ser Val
           20           25           30
Pro Phe Ser Leu Ile Tyr Ile Ile Ile Phe Leu Gly Asn Gly Ile Ile
 35           40           45
Leu His Val Ile Arg Thr Asp Ile Ala Leu His Gln Pro Met Tyr Leu
 50           55           60
Phe Leu Ala Met Leu Ala Leu Ala Glu Val Arg Val Ser Ala Ser Thr
 65           70           75           80
Leu Pro Thr Val Leu Gly Ile Phe Leu Phe Gly Asn Thr Glu Ile Ser
           85           90           95
Leu Glu Ala Phe Phe Phe Gln Met Phe Ser Ile His Ser Leu Ser Met
 100          105          110
Met Glu Ser Ala Val Leu Leu Ala Met Ser Leu Asp Arg Phe Ile Ala
 115          120          125
Ile Tyr Ser Pro Leu Ser Tyr Thr Ala Ile Leu Thr Leu Pro Arg Val
 130          135          140
Phe Gly Thr Gly Ala Ile Ile Val Leu Lys Ser Ile Met Leu Met Ala
 145          150          155          160
Pro Leu Pro Ile Leu Leu Trp Arg Leu Pro Phe Cys Gly His Asn Ala
           165          170          175
Leu Ser His Ser Tyr Cys Leu His Pro Asn Leu Ile Tyr Leu Ser Cys
 180          185          190
Gly Asn Ile Ser Val Asn Asn Ile Tyr Gly Ile Phe Ile Val Thr Ser
 195          200          205
Thr Phe Gly Leu Asp Ser Leu Leu Ile Val Ile Ser Tyr Gly Leu Ile
 210          215          220
Leu His Thr Val Leu Gly Ile Ala Thr Gly Glu Gly Arg Lys Lys Ala
 225          230          235          240
Leu Asn Thr Cys Gly Ser His Val Cys Ala Val Leu Ala Tyr Tyr Val
           245          250          255
Pro Met Ile Gly Leu Ser Ile Val His Arg Leu Gly His Arg Val Ser
 260          265          270
Pro Leu Leu Gln Ala Met Met Ala Asn Ala Tyr Leu Phe Phe Pro Pro
 275          280          285
Val Val Asn Pro Ile Val Tyr Ser Ile Lys Thr Lys Glu Ile His Gly
 290          295          300
Ala Ile Val Arg Met Leu Leu Glu Lys Arg Arg Arg Val Xaa Pro Lys
 305          310          315          320
Thr Ile Val Gly Arg Asn
           325

```

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1           5           10           15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20           25           30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35           40           45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50           55           60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
65           70           75           80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85           90           95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
          100          105          110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
          195          200          205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
          260          265          270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
          290          295          300
Val Ala His Ser Gln Gly Glu
305           310

```

&lt;210&gt; 1311

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g228 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20           25           30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
          35           40           45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
65           70           75           80

```

Met 1	Thr	Glu	Phe	Ile 5	Phe	Leu	Val	Leu	Ser 10	Pro	Asn	Gln	Glu	Val 15	Gln
Arg	Val	Cys	Phe 20	Val	Ile	Phe	Leu	Phe 25	Leu	Tyr	Thr	Ala	Ile 30	Val	Leu
Gly	Asn	Phe 35	Leu	Ile	Val	Leu	Thr 40	Val	Met	Thr	Ser	Arg 45	Ser	Leu	Gly
Ser	Pro 50	Met	Tyr	Phe	Phe	Leu 55	Ser	Tyr	Leu	Ser	Phe 60	Met	Glu	Ile	Cys
Tyr 65	Ser	Ser	Ala	Thr 70	Ala	Pro	Lys	Leu	Ile	Ser 75	Asp	Leu	Leu	Ala 80	Glu
Arg	Lys	Val	Ile	Ser 85	Trp	Trp	Gly	Cys	Met 90	Ala	Gln	Leu	Phe 95	Phe	Leu
His	Phe	Phe	Gly 100	Gly	Thr	Glu	Ile	Phe 105	Leu	Leu	Thr	Val	Met 110	Ala	Tyr
Asp	His 115	Tyr	Val	Ala	Ile	Cys	Lys 120	Pro	Leu	Ser	Tyr	Thr 125	Thr	Ile	Met
Asn	Trp 130	Gln	Val	Cys	Thr	Val 135	Leu	Val	Gly	Ile	Ala 140	Trp	Val	Gly	Gly
Phe 145	Met	His	Ser	Phe 150	Ala	Gln	Ile	Leu	Leu	Ile 155	Phe	His	Leu	Leu 160	Phe
Cys	Gly	Pro	Asn	Val	Ile	Asn	His	Tyr	Phe	Cys	Asp	Leu	Val	Pro	Leu

<div><div>&lt;400&gt;</div><div>1313</div></div>																
Leu	Ile	Ala	Thr	Gly	Asn	Trp	Thr	Arg	Ile	Ser	Glu	Phe	Ile	Leu	Met	
1				5					10					15		
Ser	Phe	Ser	Ser	Leu	Pro	Thr	Glu	Ile	Gln	Ser	Leu	Leu	Phe	Leu	Thr	
			20					25					30			
Phe	Leu	Thr	Ile	Tyr	Leu	Val	Thr	Leu	Met	Gly	Asn	Cys	Leu	Ile	Ile	
			35				40					45				
Leu	Val	Thr	Leu	Ala	Asp	Pro	Met	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	
			50			55					60					
Leu	Arg	Asn	Leu	Ser	Phe	Leu	Glu	Ile	Gly	Phe	Asn	Leu	Val	Ile	Val	
65					70					75					80	
Pro	Lys	Met	Leu	Gly	Thr	Leu	Leu	Ala	Gln	Asp	Thr	Thr	Ile	Ser	Phe	
				85					90					95		
Leu	Gly	Cys	Ala	Thr	Gln	Met	Tyr	Phe	Phe	Phe	Phe	Phe	Gly	Val	Ala	
			100					105					110			
Glu	Cys	Phe	Leu	Gln	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	
			115				120					125				
Cys	Ser	Pro	Leu	His	Tyr	Pro	Val	Ile	Met	Asn	Gln	Arg	Thr	Arg	Ala	
			130			135					140					
Lys	Leu	Ala	Ala	Ala	Ser	Trp	Phe	Pro	Gly	Phe	Pro	Val	Ala	Thr	Val	
145					150					155					160	
Gln	Thr	Thr	Trp	Leu	Phe	Ser	Phe	Pro	Phe	Cys	Gly	Thr	Asn	Lys	Val	
				165					170					175		
Asn	His	Phe	Phe	Cys	Asp	Ser	Pro	Pro	Val	Leu	Arg	Leu	Val	Cys	Ala	
			180					185					190			
Asp	Thr	Ala	Leu	Phe	Glu	Ile	Tyr	Ala	Ile	Val	Gly	Thr	Ile	Leu	Val	
			195				200					205				
Val	Met	Ile	Pro	Cys	Leu	Leu	Ile	Leu	Cys	Ser	Tyr	Thr	Arg	Ile	Ala	
			210			215					220					
Ala	Ala	Ile	Leu	Lys	Ile	Pro	Ser	Ala	Lys	Gly	Lys	Asn	Lys	Ala	Phe	
225					230					235					240	
Ser	Thr	Cys	Ser	Ser	His	Leu	Leu	Val	Val	Ser	Leu	Phe	Tyr	Ile	Ser	
				245					250					255		
Leu	Ser	Leu	Thr	Tyr	Phe	Arg	Pro	Lys	Ser	Asn	Asn	Ser	Pro	Glu	Gly	
			260					265					270			

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn  
 275 280 285  
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser  
 290 295 300  
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu  
 305 310 315

&lt;210&gt; 1314

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g231 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1314

Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr  
 1 5 10 15  
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val  
 20 25 30  
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser  
 35 40 45  
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
 50 55 60  
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu  
 65 70 75 80  
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu  
 85 90 95  
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu  
 115 120 125  
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser  
 130 135 140  
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp  
 145 150 155 160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr  
 165 170 175  
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile  
 180 185 190  
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser  
 195 200 205  
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu  
 210 215 220  
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met  
 245 250 255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
 260 265 270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr  
 290 295 300  
 Lys Thr Tyr Val Arg  
 305

&lt;210&gt; 1315

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g232 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
 50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
145           150           155           160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
225           230           235           240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
305           310           315           320

```

&lt;210&gt; 1316

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g233 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Thr Val Gly Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe  
 85 90 95  
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu  
 130 135 140  
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr  
 145 150 155 160  
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His  
 165 170 175  
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr  
 180 185 190  
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile  
 195 200 205  
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala  
 210 215 220  
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe  
 245 250 255  
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val  
 260 265 270  
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp  
 290 295 300  
 Asn Asn Leu Cys Asn Ile Phe Val  
 305 310

&lt;210&gt; 1317

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g234 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser  
 1 5 10 15  
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe  
 20 25 30  
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu  
 35 40 45  
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro  
 65 70 75 80  
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Phe Gly Ala Ala Glu  
 100 105 110  
 Cys Cys Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

```

      130              135              140
Leu Ala Ala Ala Ser Trp Phe Ser Gly Phe Ser Val Ala Thr Val Gln
145              150              155              160
Thr Thr Trp Ile Phe Ser Phe Pro Phe Cys Gly Pro Asn Arg Val Asn
      165              170              175
His Phe Phe Cys Asp Ser Pro Pro Val Ile Ala Leu Val Cys Ala Asp
      180              185              190
Thr Ser Val Phe Glu Leu Glu Ala Leu Thr Ala Thr Val Pro Phe Ile
      195              200              205
Leu Phe Pro Phe Leu Leu Ile Leu Gly Ser Tyr Val Arg Ile Leu Ser
      210              215              220
Thr Ile Phe Arg Met Pro Ser Ala Glu Gly Lys His Gln Ala Phe Ser
225              230              235              240
Thr Cys Ser Ala His Leu Leu Val Val Ser Leu Phe Tyr Ser Thr Ala
      245              250              255
Ile Leu Thr Tyr Phe Arg Pro Gln Ser Ser Ala Ser Ser Glu Ser Lys
      260              265              270
Lys Leu Leu Ser Leu Ser Ser Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Ile Ile Tyr Ser Ser Arg Asn Lys Glu Val Lys Ala Ala Leu Lys Arg
      290              295              300
Leu Ile His Arg Thr Leu Gly Ser Gln Lys Leu
305              310              315

```

&lt;210&gt; 1318

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g235 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1318

```

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
      20              25              30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
      35              40              45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
      50              55              60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn
      65              70              75              80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
      85              90              95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
      100              105              110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
      130              135              140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
      145              150              155              160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
      165              170              175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
      180              185              190

```



His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe  
 195 200 205  
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val  
 210 215 220  
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly  
 245 250 255  
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp  
 260 265 270  
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met  
 290 295 300  
 Glu Asn Leu Cys Leu Thr  
 305 310

&lt;210&gt; 1319

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g236 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(184)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr  
 1 5 10 15  
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile  
 20 25 30  
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser  
 35 40 45  
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu  
 50 55 60  
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys  
 65 70 75 80  
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His  
 85 90 95  
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile  
 100 105 110  
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His  
 115 120 125  
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val  
 130 135 140  
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys  
 145 150 155 160  
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr  
 165 170 175  
 Val Tyr Leu Gln Pro Asp Phe Phe  
 180

&lt;210&gt; 1320

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g237 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
      20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
      35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
      50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
      65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
      85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
      100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
      130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
      145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
      165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
      180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
      195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
      210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
      225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
      245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
      260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
      275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
      290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
      305          310          315          320
Lys

```

&lt;210&gt; 1321

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g238 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(134)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```

Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg  
 20 25 30  
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln  
 35 40 45  
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser  
 50 55 60  
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly  
 65 70 75 80  
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln  
 85 90 95  
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser  
 100 105 110  
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Lys Xaa Ser Gly Glu Arg  
 115 120 125  
 Ser Ser Phe Pro Arg Glu  
 130

&lt;210&gt; 1322

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g239 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro  
 20 25 30  
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn  
 35 40 45  
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser  
 65 70 75 80  
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys  
 85 90 95  
 Thr Ile Ser Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val  
 100 105 110  
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg  
 115 120 125  
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro  
 130 135 140  
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile  
 145 150 155 160  
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser  
 165 170 175  
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala  
 180 185 190  
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe  
 195 200 205  
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr  
 210 215 220  
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg  
 225 230 235 240  
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

				245					250					255			
Phe	Tyr	Gly	Thr	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Arg	Ser	Asn	His		
			260						265					270			
Ser	Leu	Asp	Thr	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Val	Ile		
		275					280						285				
Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys		
		290				295					300						
Asp	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Cys	Arg	Ser	Leu				
305					310					315							

&lt;210&gt; 1323

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g240 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1323

Met	Leu	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly		
1				5					10					15			
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu		
		20						25					30				
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu		
		35				40					45						
Ile	Arg	Thr	Asn	Ser	Gln	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly		
	50				55					60							
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn		
65				70					75					80			
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly		
			85					90						95			
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe		
		100					105					110					
Tyr	Phe	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser		
	115				120						125						
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Ile	Ser	Leu		
	130				135					140							
Val	Thr	Val	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Asn	Gly	Leu	Ser	Gln	Thr		
145				150				155						160			
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His		
			165					170						175			
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr		
		180					185					190					
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Thr	Leu	Ser		
	195				200						205						
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala		
	210				215						220						
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr		
225				230					235					240			
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe		
			245					250					255				
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys		
	260						265					270					
Ile	Ile	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu		
	275					280						285					
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Val	Ile	Leu	Ala	Ile	Gln	Gln	Met		
	290				295					300							
Ile	Arg	Gly	Lys	Ser	Phe	Cys	Lys	Ile	Ala	Val							
305				310						315							

&lt;210&gt; 1324

<211> 313  
 <212> PRT  
 <213> Unknown (H38g241 protein)

<220>  
 <223> Synthetic construct

<400> 1324

```

Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro
           20           25           30
Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe
           35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys
           50           55           60
Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile
           65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe
           85           90           95
Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met
           100          105          110
Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
           115          120          125
Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
           130          135          140
Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro
           145          150          155          160
Leu Val Phe Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
           165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
           180          185          190
Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu
           195          200          205
Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr
           210          215          220
Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
           225          230          235          240
Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala
           245          250          255
Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr
           260          265          270
Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu
           275          280          285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val
           290          295          300
Leu Arg Ile Phe Phe Lys Thr Asp His
           305          310

```

<210> 1325  
 <211> 328  
 <212> PRT  
 <213> Unknown (H38g242 protein)

<220>  
 <223> Synthetic construct

<400> 1325

```

Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr
 1           5           10           15
Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

			20					25				30			
Gln	Thr	Ile	Phe	Phe	Phe	Leu	Phe	Leu	Ala	Ile	Tyr	Leu	Phe	Thr	Leu
		35						40				45			
Met	Gly	Asn	Leu	Gly	Leu	Ile	Leu	Val	Val	Ile	Arg	Asp	Ser	Gln	Leu
		50				55					60				
His	Lys	Pro	Met	Tyr	Tyr	Phe	Leu	Ser	Met	Leu	Ser	Ser	Val	Asp	Ala
65				70						75				80	
Cys	Tyr	Ser	Ser	Val	Ile	Thr	Pro	Asn	Met	Leu	Val	Asp	Phe	Thr	Thr
				85					90					95	
Lys	Asn	Lys	Val	Ile	Ser	Phe	Leu	Gly	Cys	Val	Ala	Gln	Val	Phe	Leu
			100					105					110		
Ala	Cys	Ser	Phe	Gly	Thr	Thr	Glu	Cys	Phe	Leu	Leu	Ala	Ala	Met	Ala
		115					120					125			
Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Tyr	Asn	Pro	Leu	Leu	Tyr	Ser	Val	Ser
	130					135					140				
Met	Ser	Pro	Arg	Val	Tyr	Met	Pro	Leu	Ile	Asn	Ala	Ser	Tyr	Val	Ala
145				150						155				160	
Gly	Ile	Leu	His	Ala	Thr	Ile	His	Thr	Val	Ala	Thr	Phe	Ser	Leu	Ser
			165					170						175	
Phe	Cys	Gly	Ala	Asn	Glu	Ile	Arg	Arg	Val	Phe	Cys	Asp	Ile	Pro	Pro
			180					185					190		
Leu	Leu	Ala	Ile	Ser	Tyr	Ser	Asp	Thr	His	Thr	Asn	Gln	Leu	Leu	Leu
	195						200					205			
Phe	Tyr	Phe	Val	Gly	Ser	Ile	Glu	Leu	Val	Thr	Ile	Leu	Ile	Val	Leu
	210				215						220				
Ile	Ser	Tyr	Gly	Leu	Ile	Leu	Leu	Ala	Ile	Leu	Lys	Met	Tyr	Ser	Ala
225				230						235				240	
Glu	Gly	Arg	Arg	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ala	His	Leu	Thr	Gly
			245						250					255	
Val	Ser	Ile	Tyr	Gly	Thr	Ile	Leu	Phe	Met	Tyr	Val	Arg	Pro	Ser	
		260					265					270			
Ser	Ser	Tyr	Ala	Ser	Asp	His	Asp	Met	Ile	Val	Ser	Ile	Phe	Tyr	Thr
		275					280					285			
Ile	Val	Ile	Pro	Leu	Leu	Asn	Pro	Val	Ile	Tyr	Ser	Leu	Arg	Asn	Lys
	290					295					300				
Asp	Val	Lys	Asp	Ser	Met	Lys	Lys	Met	Phe	Gly	Lys	Asn	Gln	Val	Ile
305				310						315					320
Asn	Lys	Val	Tyr	Phe	His	Thr	Lys								
				325											

&lt;210&gt; 1326

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g243 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1326

Met	Asn	Gly	Ala	Asn	Ser	Ser	Ser	Leu	Thr	Pro	Arg	Tyr	Phe	Ile	Leu
1				5					10					15	
Ser	Gly	Val	Pro	Gly	Leu	Glu	Ala	Ala	His	Ile	Trp	Ile	Ser	Leu	Pro
		20					25					30			
Phe	Cys	Phe	Met	Tyr	Ile	Ile	Val	Val	Leu	Gly	Asn	Cys	Gly	Leu	Ile
	35					40					45				
Tyr	Leu	Ile	Ser	His	Glu	Glu	Ala	Leu	His	Gln	Pro	Thr	Tyr	Tyr	Phe
	50					55					60				

```

Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val
65          70          75          80
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe
          85          90          95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met
          100         105         110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115         120         125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr
          130         135         140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro
145          150          155          160
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile
          165         170         175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly
          180         185         190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile
          195         200         205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile
210         215         220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225         230         235         240
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro
          245         250         255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
          260         265         270
His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
275         280         285
Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
290         295         300
Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
305         310         315         320
Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
          325

```

&lt;210&gt; 1327

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g244 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(301)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1327

```

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
1          5          10          15
Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
          20          25          30
Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
          35          40          45
Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
50          55          60
Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
65          70          75          80
Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
          85          90          95
Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

```

100	105	110
Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr		
115	120	125
Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe		
130	135	140
Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val		
145	150	155
Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp		
165	170	175
Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly		
180	185	190
Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile		
195	200	205
Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser		
210	215	220
Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val		
225	230	235
Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr		
245	250	255
Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu		
260	265	270
Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met		
275	280	285
Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu		
290	295	300

&lt;210&gt; 1328

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g245 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1328

Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr	
1 5 10 15	
Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe	
20 25 30	
Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala	
35 40 45	
Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu	
50 55 60	
Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro	
65 70 75 80	
Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp	
85 90 95	
Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu	
100 105 110	
Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr	
115 120 125	
Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys	
130 135 140	
Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu	
145 150 155 160	
Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser	
165 170 175	



His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp  
 180 185 190  
 Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe  
 195 200 205  
 Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr  
 210 215 220  
 Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met  
 245 250 255  
 Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile  
 260 265 270  
 Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile  
 290 295 300  
 Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg  
 305 310 315 320  
 Ser Gln Glu Leu

&lt;210&gt; 1329

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g246 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(292)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1329

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu  
 1 5 10 15  
 Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln  
 20 25 30  
 Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr  
 35 40 45  
 Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe  
 50 55 60  
 Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu  
 65 70 75 80  
 Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg  
 85 90 95  
 Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile  
 100 105 110  
 Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu  
 115 120 125  
 Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His  
 130 135 140  
 Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val  
 145 150 155 160  
 Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile  
 165 170 175  
 Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu  
 180 185 190  
 Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys  
 195 200 205  
 Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

210		215		220
Xaa Tyr Thr Ala Trp	Xaa Lys His Pro Cys Tyr Ile Arg Ile Phe Leu			
225	230	235		240
Ala Asn Val Tyr Thr Val Val Leu Pro Val Phe Asn Pro Val Ile Tyr				
	245	250		255
Gly Ile Arg Lys Lys Gln Ile Pro Asp Xaa Gly Ile Asp Leu Lys Thr				
	260	265		270
Phe Asp Asp Gln Ser Leu Leu Val Met Met Ile Tyr Ile Leu Gly Tyr				
	275	280		285
Ile Cys Lys Tyr				
290				

&lt;210&gt; 1330

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g247 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1330

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly				
1	5	10		15
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Phe Leu Phe Ser				
	20	25		30
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr				
	35	40		45
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala				
	50	55		60
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys				
	65	70		75
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly				
	85	90		95
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met				
	100	105		110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys				
	115	120		125
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe				
	130	135		140
Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu				
	145	150		155
Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser				
	165	170		175
Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr				
	180	185		190
Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu				
	195	200		205
Ala Ser Phe Leu Ile Leu Ile Ile Ser Tyr Ile Phe Ile Leu Val Thr				
	210	215		220
Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu				
	225	230		235
Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe				
	245	250		255
Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala				
	260	265		270
Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr				
	275	280		285
Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Cys Ser Gln				
	290	295		300
Phe Val Asn Tyr Ser Lys Ile Phe				
305	310			

<210> 1331  
 <211> 168  
 <212> PRT  
 <213> Unknown (H38g248 protein)

<220>  
 <223> Synthetic construct

<400> 1331

```

Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1          5          10          15
Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
          20          25          30
Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
          35          40          45
Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
          50          55          60
Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
65          70          75          80
Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
          85          90          95
Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
          100          105          110
Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
          130          135          140
Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
145          150          155          160
Thr Met Ala Leu Ala Ala Pro Leu
          165

```

<210> 1332  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g249 protein)

<220>  
 <223> Synthetic construct

<400> 1332

```

Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu
 1          5          10          15
Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro
          20          25          30
Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu
          35          40          45
Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe
          50          55          60
Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile
65          70          75          80
Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe
          85          90          95
Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met
          100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala
          130          135          140
Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro

```

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145          150          155          160
Phe Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu
          165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly
          180          185          190
Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
          195          200          205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
          210          215          220
Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
225          230          235          240
Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
          245          250          255
Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
          260          265          270
Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
          290          295          300
Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
305          310          315          320
Met

```

&lt;210&gt; 1333

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g250 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1333

```

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
1          5          10          15
Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
          20          25          30
Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
          35          40          45
Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
          50          55          60
Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr
65          70          75          80
Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
          85          90          95
Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
          100          105          110
Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
130          135          140
Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
145          150          155          160
Leu Pro Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn
          165          170          175
Val Ile Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser
          180          185          190
Cys Asp Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp
195          200          205
Thr Leu Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe
210          215          220

```

```

Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser
          245          250          255
Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val
          260          265          270
Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro
          275          280          285
Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys
          290          295          300
Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys
305          310          315

```

&lt;210&gt; 1334

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g251 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(302)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1334

```

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu
1      5      10      15
Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu
20     25     30
Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu
35     40     45
Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe
50     55     60
Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val
65     70     75     80
Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe
85     90     95
Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr
100    105    110
Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val
115    120    125
Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu
130    135    140
Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile
145    150    155    160
Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys
165    170    175
Tyr Phe Ser Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met
180    185    190
Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser
195    200    205
Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro
210    215    220
Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu
225    230    235    240
Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys
245    250    255
Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
260    265    270
Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

```

		275					280					285			
Thr	Phe	Gly	Thr	Ser	Ser	Xaa	Arg	Phe	Thr	Ile	Pro	Leu	Leu		
	290						295					300			

<210> 1335  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g252 protein)

<220>  
 <223> Synthetic construct

<400> 1335

Met	Pro	Leu	Phe	Asn	Ser	Leu	Cys	Trp	Phe	Pro	Thr	Ile	His	Val	Thr
1				5					10					15	
Pro	Pro	Ser	Phe	Ile	Leu	Asn	Gly	Ile	Pro	Gly	Leu	Glu	Arg	Val	His
			20					25					30		
Val	Trp	Ile	Ser	Leu	Pro	Leu	Cys	Thr	Met	Tyr	Ile	Ile	Phe	Leu	Val
		35					40					45			
Gly	Asn	Leu	Gly	Leu	Val	Tyr	Leu	Ile	Tyr	Tyr	Glu	Glu	Ser	Leu	His
	50					55					60				
His	Pro	Met	Tyr	Phe	Phe	Phe	Gly	His	Ala	Leu	Ser	Leu	Ile	Asp	Leu
65					70					75					80
Leu	Thr	Cys	Thr	Thr	Thr	Leu	Pro	Asn	Ala	Leu	Cys	Ile	Phe	Trp	Phe
				85					90					95	
Ser	Leu	Lys	Glu	Ile	Asn	Phe	Asn	Ala	Cys	Leu	Ala	Gln	Met	Phe	Phe
			100					105					110		
Val	His	Gly	Phe	Thr	Gly	Val	Glu	Ser	Gly	Val	Leu	Met	Leu	Met	Ala
		115					120					125			
Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Tyr	Pro	Leu	Arg	Tyr	Ala	Thr	Thr
	130					135					140				
Leu	Thr	Asn	Pro	Ile	Ile	Ala	Lys	Ala	Glu	Leu	Ala	Thr	Phe	Leu	Arg
145					150					155					160
Gly	Val	Leu	Leu	Met	Ile	Pro	Phe	Pro	Phe	Leu	Val	Lys	Arg	Leu	Pro
				165					170					175	
Phe	Cys	Gln	Ser	Asn	Ile	Ile	Ser	His	Thr	Tyr	Cys	Asp	His	Met	Ser
			180					185					190		
Val	Val	Lys	Leu	Ser	Cys	Ala	Ser	Ile	Lys	Val	Asn	Val	Ile	Tyr	Gly
		195					200					205			
Leu	Met	Val	Ala	Leu	Leu	Ile	Gly	Val	Phe	Asp	Ile	Cys	Cys	Ile	Ser
	210					215					220				
Leu	Ser	Tyr	Thr	Leu	Ile	Leu	Lys	Ala	Ala	Ile	Ser	Leu	Ser	Ser	Ser
225					230					235					240
Asp	Ala	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys	Thr	Ala	His	Ile	Ser	Ala
				245					250					255	
Ile	Ile	Ile	Thr	Tyr	Val	Pro	Ala	Phe	Phe	Thr	Phe	Phe	Ala	His	Arg
			260					265					270		
Phe	Gly	Gly	His	Thr	Ile	Pro	Pro	Ser	Leu	His	Ile	Ile	Val	Ala	Asn
	275						280					285			
Leu	Tyr	Leu	Leu	Leu	Pro	Pro	Thr	Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val
	290					295					300				
Lys	Thr	Lys	Gln	Ile	Arg	Lys	Ser	Val	Ile	Lys	Phe	Phe	Gln	Gly	Asp
305					310					315					320
Lys	Gly	Ala	Gly												

<210> 1336  
 <211> 274  
 <212> PRT  
 <213> Unknown (H38g253 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(274)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1336

```

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1           5           10           15
Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
          20           25           30
Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
      35           40           45
Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
      50           55           60
Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
65           70           75           80
Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
          85           90           95
Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
          100          105          110
Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
      115          120          125
Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
      130          135          140
Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
145          150          155          160
Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
          165          170          175
Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
      180          185          190
Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
      195          200          205
Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
      210          215          220
Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
225          230          235          240
Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
          245          250          255
Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
          260          265          270
Ile Leu

```

&lt;210&gt; 1337

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g254 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1337

```

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

```

<210> 1338  
<211> 323  
<212> PRT  
<213> Unknown (H38g255 protein)

```
<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid
```

<400> 1338															
Val	Glu	Asn	Ser	Pro	Met	Val	Thr	Asp	Phe	Ile	Phe	Leu	Gly	Met	Thr
1				5					10					15	
Asp	Asn	Ser	Gln	Leu	Glu	Val	Leu	Leu	Phe	Gly	Val	Phe	Leu	Ile	Ala
			20					25					30		
Tyr	Ile	Ile	Thr	Val	Leu	Glu	Asn	Leu	Gly	Leu	Val	Val	Leu	Ile	Arg
		35					40					45			
Val	Ser	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn	Gln
	50					55					60				
Ser	Phe	Leu	Asp	Val	Cys	Phe	Ser	Ser	Ile	Thr	Ile	Pro	Gln	Asn	Leu
65					70					75					80



Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr  
                     85                    90                    95  
 Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe  
                     100                    105                    110  
 Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu  
                     115                    120                    125  
 Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala  
                     130                    135                    140  
 Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser  
 145                    150                    155                    160  
 Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe  
                     165                    170                    175  
 Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile  
                     180                    185                    190  
 Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr  
                     195                    200                    205  
 Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile  
                     210                    215                    220  
 Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys  
 225                    230                    235                    240  
 Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr  
                     245                    250                    255  
 Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile  
                     260                    265                    270  
 Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile  
                     275                    280                    285  
 Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu  
                     290                    295                    300  
 Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile  
 305                    310                    315                    320  
 Leu Xaa Arg

&lt;210&gt; 1339

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g256 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1339

Trp Leu Asp Glu Lys Lys Gln Asp Ser Asn Val Thr Glu Leu Val Leu  
 1                    5                    10                    15  
 Leu Gly Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Leu Leu  
                     20                    25                    30  
 Phe Leu Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val  
                     35                    40                    45  
 Val Thr Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr  
                     50                    55                    60  
 Phe Leu Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr  
 65                    70                    75                    80  
 Leu Pro Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser  
                     85                    90                    95  
 Phe Ser Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala  
                     100                    105                    110  
 Ser Glu Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala  
                     115                    120                    125  
 Ile Cys Asn Pro Leu Arg Tyr Leu Ile Ile Met Asn Pro Gln Leu Cys  
                     130                    135                    140  
 Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
          165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
          180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
          195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
          210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
          245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
          260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
          290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

&lt;210&gt; 1340

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g257 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
 1          5          10          15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
          20          25          30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
          35          40          45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
          50          55          60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65          70          75          80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
          85          90          95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
          100          105          110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
          115          120          125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
          130          135          140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145          150          155          160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
          165          170          175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
          180          185          190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
          195          200          205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
          210          215          220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225          230          235          240

```

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
 245 250 255  
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
 260 265 270  
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
 290 295 300  
 Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
 305 310 315

&lt;210&gt; 1341

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g258 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1341

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe  
 1 5 10 15  
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln  
 20 25 30  
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met  
 35 40 45  
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His  
 50 55 60  
 Thr Pro Met Tyr Thr Leu Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp  
 65 70 75 80  
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys  
 85 90 95  
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu  
 100 105 110  
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln  
 130 135 140  
 Val Cys Thr Gly Leu Ile Phe Ala Trp Ser Cys Val Phe Val Ile  
 145 150 155 160  
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro  
 165 170 175  
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu  
 180 185 190  
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe  
 195 200 205  
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr  
 210 215 220  
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys  
 225 230 235 240  
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu  
 245 250 255  
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His  
 260 265 270  
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr  
 275 280 285  
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys

290		295		300
Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile				
305		310		315
				320

<210> 1342  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g259 protein)

<220>  
 <223> Synthetic construct

<400> 1342

Met	Leu	Asn	Thr	Thr	Ser	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Val	Thr
1				5					10					15	
Asp	Ile	Gln	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Val	Val	Phe	Leu	Thr	Ile
		20						25					30		
Tyr	Phe	Ile	Ser	Val	Ala	Gly	Asn	Gly	Ala	Ile	Leu	Met	Ile	Val	Ile
		35					40					45			
Ser	Asp	Pro	Arg	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn	Leu
	50					55					60				
Ser	Cys	Leu	Asp	Ile	Cys	Tyr	Ser	Ser	Val	Thr	Leu	Pro	Lys	Met	Leu
65				70						75					80
Gln	Asn	Phe	Leu	Ser	Ala	His	Lys	Ala	Ile	Ser	Phe	Leu	Gly	Cys	Ile
			85						90					95	
Ser	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly	Ser	Thr	Glu	Ala	Met	Leu
			100					105					110		
Leu	Ala	Val	Met	Ala	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	Lys	Pro	Leu
	115						120					125			
Arg	Tyr	Thr	Val	Ile	Met	Asn	Pro	Gln	Leu	Cys	Thr	Gln	Met	Ala	Ile
	130					135					140				
Thr	Ile	Trp	Met	Ile	Gly	Phe	Phe	His	Ala	Leu	Leu	His	Ser	Leu	Met
145				150						155					160
Thr	Ser	Arg	Leu	Asn	Phe	Cys	Gly	Ser	Asn	Arg	Ile	Tyr	His	Phe	Phe
			165						170					175	
Cys	Asp	Val	Lys	Pro	Leu	Leu	Lys	Leu	Ser	Leu	Ile	Ser	Gly	Trp	Leu
		180						185					190		
Ser	Thr	Val	Thr	Gly	Thr	Ile	Ala	Met	Gly	Pro	Phe	Phe	Leu	Thr	Leu
	195						200					205			
Leu	Ser	Tyr	Phe	Tyr	Ile	Ile	Thr	His	Leu	Phe	Phe	Lys	Thr	His	Ser
	210					215					220				
Phe	Ser	Met	Leu	Arg	Lys	Ala	Leu	Ser	Thr	Cys	Ala	Ser	His	Phe	Met
225					230					235					240
Val	Val	Ile	Leu	Leu	Tyr	Ala	Pro	Val	Leu	Phe	Thr	Tyr	Ile	His	His
			245						250					255	
Ala	Ser	Gly	Thr	Ser	Met	Asp	Gln	Asp	Arg	Ile	Thr	Ala	Ile	Met	Tyr
		260						265					270		
Thr	Val	Val	Thr	Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn
		275					280					285			
Lys	Glu	Val	Lys	Gly	Ala	Phe	Asn	Arg	Ala	Met	Lys	Arg	Trp	Leu	Trp
	290					295					300				
Pro	Lys	Glu	Ile	Leu											
305															

<210> 1343  
 <211> 331  
 <212> PRT  
 <213> Unknown (H38g260 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Leu Val Phe Val Leu Val Leu
           20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
           35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
           50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
           85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
           100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
           115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
           130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145           150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
           165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
           180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
           195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
210           215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225           230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
           245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
           260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
           275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
290           295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
305           310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
           325          330

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&lt;210&gt; 1344

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g261 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

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<210> 1345
<211> 312
<212> PRT
<213> Unknown (H38g262 protein)
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<220>  
<223> Synthetic construct

Met	Ser	Ala	Asn	Thr	Ser	Met	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Phe
1				5					10					15	
Ser	His	Leu	Ala	Asp	Leu	Gln	Gly	Leu	Leu	Phe	Ser	Val	Phe	Leu	Thr
			20					25					30		
Ile	Tyr	Leu	Leu	Thr	Val	Ala	Gly	Asn	Phe	Leu	Ile	Val	Val	Leu	Val
			35				40					45			
Ser	Thr	Asp	Ala	Ala	Leu	Gln	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Arg	Thr
	50					55					60				
Leu	Ser	Ala	Leu	Glu	Ile	Gly	Tyr	Thr	Ser	Val	Thr	Val	Pro	Leu	Leu
65				70						75				80	
Leu	His	His	Leu	Leu	Thr	Gly	Arg	Arg	His	Ile	Ser	Arg	Ser	Gly	Cys
				85					90					95	
Ala	Leu	Gln	Met	Phe	Phe	Phe	Leu	Phe	Phe	Gly	Ala	Thr	Glu	Cys	Cys
			100					105					110		

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro  
 115 120 125  
 Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala  
 130 135 140  
 Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro  
 145 150 155 160  
 Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe  
 165 170 175  
 Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser  
 180 185 190  
 Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys  
 195 200 205  
 Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile  
 210 215 220  
 Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe  
 245 250 255  
 Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu  
 260 265 270  
 Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile  
 290 295 300  
 Gln Lys Thr Val Pro Met Glu Ile  
 305 310

&lt;210&gt; 1346

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g263 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1346

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser  
 1 5 10 15  
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser  
 20 25 30  
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val  
 35 40 45  
 Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu  
 50 55 60  
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu  
 65 70 75 80  
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser  
 85 90 95  
 Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu  
 100 105 110  
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu  
 115 120 125  
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser  
 130 135 140  
 Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser  
 145 150 155 160  
 Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu  
 165 170 175  
 Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr  
 180 185 190  
 Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

	195		200		205										
Leu	Ser	Leu	Ile	Leu	Ala	Ser	Tyr	Gly	Ala	Thr	Ala	Gln	Ala	Val	Leu
	210					215					220				
Arg	Ile	Asn	Ser	Ala	Thr	Ala	Trp	Arg	Lys	Ala	Phe	Gly	Thr	Cys	Ser
225					230					235					240
Ser	His	Leu	Thr	Val	Val	Thr	Leu	Phe	Tyr	Ser	Ser	Val	Ile	Ala	Val
				245					250					255	
Tyr	Leu	Gln	Pro	Lys	Asn	Pro	Tyr	Ala	Gln	Gly	Arg	Gly	Lys	Phe	Phe
			260					265					270		
Gly	Leu	Phe	Tyr	Ala	Val	Gly	Thr	Pro	Ser	Leu	Asn	Pro	Leu	Val	Tyr
		275					280					285			
Thr	Leu	Arg	Asn	Lys	Glu	Ile	Lys	Arg	Ala	Leu	Arg	Arg	Leu	Leu	Gly
	290					295					300				
Lys	Glu	Arg	Asp	Ser	Arg	Glu	Ser	Trp	Arg	Ala	Ala				
305					310					315					

&lt;210&gt; 1347

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g264 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1347

Met	Lys	Ser	Glu	Leu	Asn	Arg	Asn	Tyr	Ser	Glu	Val	Thr	Glu	Phe	Ile
1				5				10						15	
Leu	Leu	Gly	Phe	Arg	Thr	Ser	Pro	Glu	Ala	Gln	Ile	Leu	Leu	Phe	Phe
			20					25					30		
Leu	Phe	Leu	Leu	Ile	Tyr	Met	Val	Ile	Val	Leu	Arg	Asn	Leu	Ser	Met
		35				40						45			
Leu	Val	Val	Ile	Glu	Ile	Asp	Ser	Arg	Leu	His	Thr	Pro	Val	Tyr	Phe
	50					55					60				
Phe	Leu	Arg	Asn	Leu	Ser	Tyr	Leu	Asp	Leu	Arg	Tyr	Ser	Thr	Val	Ile
65					70					75				80	
Ala	Pro	Lys	Leu	Thr	Thr	Leu	Phe	Ser	Lys	Glu	Lys	Lys	Ile	Ser	Tyr
				85				90						95	
Asn	Gly	Xaa	Ala	Thr	Gln	Leu	Phe	Phe	Phe	Ala	Leu	Phe	Val	Gly	Thr
			100					105					110		
Glu	Gly	Phe	Phe	Leu	Asp	Met	Met	Ala	Tyr	Asp	Arg	Phe	Ser	Ala	Ile
		115				120						125			
Cys	Ser	Pro	Phe	Phe	Tyr	Thr	Val	Cys	Met	Ser	Gln	Gln	Ala	Cys	Val
	130					135					140				
Cys	Leu	Val	Val	Gly	Ser	Ser	Ile	Cys	Gly	Cys	Ile	Asn	Ser	Met	Ile
145					150					155				160	
Gln	Thr	Gly	Phe	Thr	Phe	Ser	Leu	His	Phe	Cys	Gly	Glu	Asn	Arg	Leu
				165					170					175	
Glu	His	Phe	Phe	Cys	Asp	Val	Ser	Val	Met	Ile	Lys	Ile	Ser	Cys	Ile
		180						185					190		
Asp	Ile	Leu	Val	Asn	Glu	Val	Val	Leu	Phe	Ile	Leu	Ser	Ala	Leu	Ile
		195					200					205			
Thr	Thr	Thr	Thr	Thr	Val	Ile	Leu	Ala	Ser	Tyr	Val	His	Ile	Leu	Ser
	210					215					220				
Thr	Val	Leu	Lys	Ile	Leu	Ser	Thr	His	Gly	Arg	Arg	Lys	Thr	Phe	Ser
225					230					235				240	
Thr	Cys	Ser	Ser	His	Ile	Thr	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Val
				245					250					255	



Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile  
                   260                  265                  270  
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr  
                   275                  280                  285  
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys  
                   290                  295                  300  
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile  
                   305                  310                  315

&lt;210&gt; 1348

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g265 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu  
   1                  5                  10                  15  
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro  
                   20                  25                  30  
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
                   35                  40                  45  
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val  
                   50                  55                  60  
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu  
   65                  70                  75                  80  
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly  
                   85                  90                  95  
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val  
                   100                  105                  110  
 Leu Leu Phe Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro  
                   115                  120                  125  
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr  
                   130                  135                  140  
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys  
   145                  150                  155                  160  
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile  
                   165                  170                  175  
 Ser

&lt;210&gt; 1349

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g266 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly  
   1                  5                  10                  15  
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu  
                   20                  25                  30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
                   35                  40                  45  
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
                   50                  55                  60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65      70      75      80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
      130      135      140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145      150      155      160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165      170      175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
      180      185      190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Gly Val
      195      200      205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
      210      215      220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
225      230      235      240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
      260      265      270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
      290      295      300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
305      310      315      320
Lys Arg

```

<210> 1350  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g267 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(322)  
 <223> Xaa = Any Amino Acid

```

<400> 1350
Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
      20      25      30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
      85      90      95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
      100      105      110

```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Gln Val Ile Met Ser Pro Arg Leu Cys Gly Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp  
 180 185 190  
 Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly  
 195 200 205  
 Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser  
 210 215 220  
 Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala  
 245 250 255  
 Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly  
 260 265 270  
 Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg  
 290 295 300  
 Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys  
 305 310 315 320  
 Ser Ile

&lt;210&gt; 1351

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g268 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1351

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu  
 20 25 30  
 Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu  
 35 40 45  
 Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln  
 65 70 75 80  
 Ala Leu Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu  
 85 90 95  
 Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys  
 100 105 110  
 Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu  
 130 135 140  
 Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr  
 145 150 155 160  
 Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His  
 165 170 175  
 Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

<210> 1352  
<211> 321  
<212> PRT  
<213> Unknown (H38g269 protein)

<220>  
<223> Synthetic construct

Met 1	Pro 5	Ile 10	Leu 15	Met 20	Ala 25	Ile 30	Gly 35	Asn 40	Trp 45	Thr 50	Glu 55	Ile 60	Ser 65	Glu 70	Phe 75
Ile	Leu	Met	Ser	Phe	Ser	Ser	Leu	Pro	Thr	Glu	Ile	Gln	Ser	Leu	Leu
Phe	Leu	Thr	Phe	Leu	Thr	Ile	Tyr	Leu	Val	Thr	Leu	Lys	Gly	Asn	Ser
Leu	Ile	Ile	Leu	Val	Thr	Leu	Ala	Asp	Pro	Met	Leu	His	Ser	Pro	Met
Tyr 65	Phe	Phe	Leu	Arg	Asn 70	Leu	Ser	Phe	Leu	Glu 75	Ile	Gly	Phe	Asn	Leu 80
Val	Ile	Val	Pro	Lys 85	Met	Leu	Gly	Thr	Leu 90	Leu	Ala	Gln	Asp	Thr 95	Thr
Ile	Ser	Phe	Leu	Gly 100	Cys	Ala	Thr	Gln 105	Met	Tyr	Phe	Phe	Phe 110	Phe	Phe
Gly	Val	Ala	Glu	Cys 115	Phe	Leu	Leu	Ala 120	Thr	Met	Ala	Tyr	Asp	Arg	Tyr
Val	Ala	Ile	Cys	Ser 130	Pro	Leu 135	His	Tyr	Pro	Val	Ile 140	Met	Asn	Gln	Arg
Thr 145	Arg	Ala	Lys	Leu 150	Ala	Ala	Ala	Ser	Trp	Phe 155	Pro	Gly	Phe	Pro	Val 160
Ala	Thr	Val	Gln	Thr 165	Thr	Trp	Leu	Phe 170	Ser	Phe	Pro	Phe	Cys	Gly 175	Thr
Asn	Lys	Val	Asn 180	His	Phe	Phe	Cys	Asp 185	Ser	Pro	Pro	Val	Leu 190	Lys	Leu
Val	Cys	Ala	Asp 195	Thr	Ala	Leu	Phe 200	Glu	Ile	Tyr	Ala	Ile 205	Val	Gly	Thr
Ile	Leu	Val	Val 210	Met	Ile	Pro 215	Cys	Leu	Leu	Ile	Leu 220	Cys	Ser	Tyr	Thr
Arg 225	Ile	Ala	Ala	Ala 230	Ile	Leu	Lys	Ile	Pro	Ser 235	Ala	Lys	Gly	Lys	His 240
Lys	Ala	Phe	Ser	Thr 245	Cys	Ser	Ser	His	Leu 250	Leu	Val	Val	Ser	Leu 255	Phe
Tyr	Ile	Ser	Ser 260	Ser	Leu	Thr	Tyr	Phe 265	Trp	Pro	Lys	Ser	Asn 270	Asn	Ser

Pro Glu Ser Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro  
           275                                  280                                  285  
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn  
           290                                  295                                  300  
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile  
 305                                  310                                  315                                  320  
 Pro

&lt;210&gt; 1353

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g270 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(260)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro  
   1                                  5                                  10                                  15  
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met  
                                   20                                  25                                  30  
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu  
                                   35                                  40                                  45  
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys  
   50                                  55                                  60  
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly  
 65                                  70                                  75                                  80  
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gly Gln Leu Leu Gly His  
                                   85                                  90                                  95  
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp  
                                   100                                  105                                  110  
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser  
                                   115                                  120                                  125  
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val  
                                   130                                  135                                  140  
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg  
 145                                  150                                  155                                  160  
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly  
                                   165                                  170                                  175  
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile  
                                   180                                  185                                  190  
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly  
                                   195                                  200                                  205  
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro  
   210                                  215                                  220  
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg  
 225                                  230                                  235                                  240  
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His  
                                   245                                  250                                  255  
 Leu Thr Ser Leu  
                                   260

&lt;210&gt; 1354

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g271 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1354

Glu	Glu	Ile	Leu	Xaa	Ile	Ile	Ser	Gln	His	Val	His	Thr	Gly	Cys	Val
1				5					10					15	
Gln	Asn	Xaa	Glu	Leu	Gln	Pro	Ile	Leu	Phe	Gly	Leu	Phe	Leu	Ser	Met
			20					25					30		
Cys	Leu	Val	Met	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	Val	Ser
		35					40					45			
Ser	Asp	Ser	His	Leu	His	Thr	Pro	Thr	Tyr	Phe	Phe	Leu	Ser	Asn	Leu
	50					55					60				
Ser	Leu	Ala	Asp	Ile	Gly	Phe	Pro	Ser	Thr	Thr	Val	Pro	Lys	Met	Ile
65					70					75					80
Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu
				85					90					95	
Thr	Gln	Ile	Ser	Leu	Phe	Ala	Val	Phe	Gly	Cys	Met	Glu	Asp	Met	Leu
			100					105					110		
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
		115				120						125			
Asp	Tyr	Pro	Val	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu
	130					135					140				
Leu	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Phe	Gln	Leu	His	Asn	Trp	Ile
145					150					155					160
Ala	Leu	Gln	Ile	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Ser	Phe	Phe
				165					170					175	
Cys	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr
			180					185					190		
Asn	Asn	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile	Leu	Gly	Phe	Leu	Pro
		195					200					205			
Ile	Ser	Gly	Ile	Phe	Tyr	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu
	210					215					220				
Lys	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly
225					230					235					240
Ser	His	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Ala	Leu	Gly	Gly
				245					250					255	
Tyr	Leu	Ser	Ser	Asp	Met	Ser	Ser	Tyr	Pro	Arg	Lys	Gly	Ala	Val	Ala
			260					265					270		
Ser	Val	Met	Tyr	Thr	Val	Val	Ala	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr
		275					280					285			
Ser	Leu	Arg	Lys	Arg	Asp	Ile	Lys	Ser	Ala	Leu	Gln	Gln	Leu	His	Gly
	290					295					300				
Arg	Ile	Val	Xaa	Ser	His	Asp	Leu	Ile	Ile	Gly	Ser	Ile	Leu	Xaa	Pro
305					310					315					320
Trp	Val	Gly	Lys	Gly	Ser	Lys	Val	Lys							
				325											

&lt;210&gt; 1355

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g272 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
          20          25          30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
          35          40          45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
65          70          75          80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
          85          90          95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
          100          105          110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
          130          135          140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
145          150          155          160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
          165          170          175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
          180          185          190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
          195          200          205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
          210          215          220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
225          230          235          240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
          245          250          255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
          260          265          270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
          275          280          285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
          290          295          300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
305          310          315          320
Glu

```

&lt;210&gt; 1356

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g273 protein)

&lt;220&gt;.

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1356

```

Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Leu Phe Ala
          20          25          30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

35	40	45
Ile Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe		
50	55	60
Phe Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr		
65	70	75
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly		80
	85	90
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu		95
100	105	110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp		
115	120	125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser		
130	135	140
Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe		
145	150	155
Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys		
	165	170
Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu		175
180	185	190
Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile		
195	200	205
Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser		
210	215	220
Tyr Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly		
225	230	235
Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile		
	245	250
Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu		255
260	265	270
Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile		
275	280	285
Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val		
290	295	300
Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro		
305	310	315
Asp Pro Lys Lys Ala Ser Arg		320
325		

&lt;210&gt; 1357

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g274 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1357

Met Glu Ala Gly Asn Gln Thr Gly Phe Leu Glu Phe Ile Leu Leu Gly	
1	5
Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu	10
20	25
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala	30
35	40
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser	45
50	55
Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys	60
65	70
Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp	75
	85
Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr	90
100	105
	110



Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu  
 130 135 140  
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile  
 145 150 155 160  
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val  
 195 200 205  
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser  
 210 215 220  
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu  
 290 295 300  
 Leu Ser Arg Ala Ala Ser Cys Leu  
 305 310

&lt;210&gt; 1358

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g275 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu  
 1 5 10 15  
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu  
 35 40 45  
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu  
 50 55 60  
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile  
 65 70 75 80  
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr  
 85 90 95  
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met  
 100 105 110  
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile  
 115 120 125  
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly  
 130 135 140  
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro  
 145 150 155 160  
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

Pro	Thr	Thr	Ser	165	Glu	His	Met	Ala	170	Val	Val	Lys	Met	175	Val	Cys	Val
			180	Asn	Arg	Ile	Tyr	185	Gly	Leu	Val	Val	Ala	190	Leu	Leu	Val
Asp	Thr	Thr	Val	195			200						205				
Ala	Gly	Tyr	Asp	Leu	Ser	Ala	Ile	Ala	Ser	Ser	Tyr	Val	Leu	Ile	Ile		
	210					215					220						
Gln	Ala	Ile	Met	His	Leu	Ser	Ser	Lys	Glu	Ala	His	His	Lys	Ala	Val		
225				230						235					240		
Asn	Thr	Cys	Thr	Thr	His	Ile	Cys	Val	Met	Leu	Ile	Ser	Tyr	Thr	Pro		
			245						250					255			
Ser	Leu	Phe	Ser	Phe	Leu	Ala	His	Arg	Phe	Gly	Gln	Gly	Ile	Pro	Pro		
			260					265					270				
His	Val	His	Ile	Ile	Leu	Gly	Asn	Leu	Tyr	Phe	Leu	Val	Pro	Pro	Met		
	275						280					285					
Leu	Ser	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys	Glu	Phe	Trp	Asp	Lys		
	290					295					300						
Val	Thr	Lys	Xaa	Val	Ala	Gly	Lys	Lys	Asn	Pro	Gln	Pro	Leu	Thr	Met		
305				310						315					320		

&lt;210&gt; 1359

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g276 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1359

Met	Glu	Leu	Trp	Asn	Phe	Thr	Leu	Gly	Ser	Gly	Phe	Ile	Leu	Val	Gly
1			5					10					15		
Ile	Leu	Asn	Asp	Ser	Gly	Ser	Pro	Glu	Leu	Leu	Cys	Ala	Thr	Ile	Thr
		20					25					30			
Ile	Leu	Tyr	Leu	Leu	Ala	Leu	Ile	Ser	Asn	Gly	Leu	Leu	Leu	Leu	Ala
	35					40					45				
Ile	Thr	Met	Glu	Ala	Arg	Leu	His	Met	Pro	Met	Tyr	Leu	Leu	Leu	Gly
	50				55					60					
Gln	Leu	Ser	Leu	Met	Asp	Leu	Leu	Phe	Thr	Ser	Val	Val	Thr	Pro	Lys
65				70					75					80	
Ala	Leu	Ala	Asp	Phe	Leu	Arg	Arg	Glu	Asn	Thr	Ile	Ser	Phe	Gly	Gly
			85					90					95		
Cys	Ala	Leu	Gln	Met	Phe	Leu	Ala	Leu	Thr	Met	Gly	Gly	Ala	Glu	Asp
		100					105					110			
Leu	Leu	Leu	Ala	Phe	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
	115					120					125				
Pro	Leu	Thr	Tyr	Met	Thr	Leu	Met	Ser	Ser	Arg	Ala	Cys	Trp	Leu	Met
	130				135					140					
Val	Ala	Thr	Ser	Trp	Ile	Leu	Ala	Ser	Leu	Ser	Ala	Leu	Ile	Tyr	Thr
145					150				155					160	
Val	Tyr	Thr	Met	His	Tyr	Pro	Phe	Cys	Arg	Ala	Gln	Glu	Ile	Arg	His
			165					170					175		
Leu	Leu	Cys	Glu	Ile	Pro	His	Leu	Leu	Lys	Val	Ala	Cys	Ala	Asp	Thr
		180					185					190			
Ser	Arg	Tyr	Glu	Leu	Met	Val	Tyr	Val	Met	Gly	Val	Thr	Phe	Leu	Ile
	195					200					205				
Pro	Ser	Leu	Ala	Ala	Ile	Leu	Ala	Ser	Tyr	Thr	Gln	Ile	Leu	Leu	Thr
	210				215					220					
Val	Leu	His	Met	Pro	Ser	Asn	Glu	Gly	Arg	Lys	Lys	Ala	Leu	Val	Thr
225				230					235					240	
Cys	Ser	Ser	His	Leu	Thr	Val	Val	Gly	Met	Phe	Tyr	Gly	Ala	Ala	Thr
			245					250					255		

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn  
 260 265 270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val  
 290 295 300  
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu  
 305 310 315

<210> 1360

<211> 312

<212> PRT

<213> Unknown (H38g277 protein)

<220>

<223> Synthetic construct

<400> 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly  
 1 5 10 15  
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn  
 100 105 110  
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu  
 130 135 140  
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr  
 145 150 155 160  
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val  
 180 185 190  
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val  
 195 200 205  
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser  
 210 215 220  
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile  
 225 230 235 240  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe  
 245 250 255  
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala  
 260 265 270  
 Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu  
 290 295 300  
 Ile Ser Arg Ile Pro Ser Phe His  
 305 310

<210> 1361

<211> 328

<212> PRT  
 <213> Unknown (H38g278 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(328)  
 <223> Xaa = Any Amino Acid

<400> 1361

Lys	Ile	Ser	Asn	Ser	Ser	Lys	Phe	Gln	Val	Ser	Glu	Phe	Ile	Leu	Leu
1				5					10					15	
Gly	Phe	Pro	Gly	Ile	His	Ser	Trp	Gln	His	Trp	Leu	Ser	Leu	Pro	Leu
			20					25					30		
Ala	Leu	Leu	Tyr	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Thr	Leu	Ile	Leu	Ile
		35					40					45			
Ile	Ile	Trp	Gln	Asn	Pro	Ser	Leu	Gln	Gln	Pro	Met	Tyr	Ile	Phe	Leu
	50					55					60				
Gly	Ile	Leu	Cys	Met	Val	Asp	Met	Gly	Leu	Ala	Thr	Thr	Ile	Ile	Pro
65				70						75					80
Lys	Ile	Leu	Ala	Ile	Phe	Trp	Phe	Asp	Ala	Lys	Val	Ile	Ser	Leu	Pro
			85						90					95	
Glu	Cys	Phe	Ala	Gln	Ile	Tyr	Ala	Ile	His	Phe	Phe	Val	Gly	Met	Glu
			100				105						110		
Ser	Gly	Ile	Leu	Leu	Cys	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	Cys
			115				120					125			
His	Pro	Leu	Arg	Tyr	Pro	Ser	Ile	Val	Thr	Ser	Ser	Leu	Ile	Leu	Lys
	130					135						140			
Ala	Thr	Leu	Phe	Met	Val	Leu	Arg	Asn	Gly	Leu	Phe	Val	Thr	Pro	Val
145					150					155					160
Pro	Val	Leu	Ala	Ala	Gln	Arg	Asp	Tyr	Cys	Ser	Lys	Asn	Glu	Ile	Glu
			165						170					175	
His	Cys	Leu	Cys	Ser	Asn	Leu	Gly	Val	Thr	Ser	Leu	Ala	Cys	Asp	Asp
		180					185						190		
Arg	Arg	Pro	Asn	Ser	Ile	Cys	Gln	Leu	Val	Leu	Ala	Trp	Leu	Gly	Met
		195					200					205			
Gly	Ser	Asp	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Tyr	Ile	Leu	Ile	Leu	Tyr
	210					215					220				
Ser	Val	Leu	Arg	Leu	Asn	Ser	Ala	Glu	Ala	Ala	Ala	Lys	Ala	Leu	Ser
225					230				235						240
Thr	Cys	Ser	Ser	His	Leu	Thr	Leu	Ile	Leu	Phe	Phe	Tyr	Thr	Ile	Val
			245						250					255	
Val	Val	Ile	Ser	Val	Thr	His	Leu	Thr	Glu	Met	Lys	Ala	Thr	Leu	Ile
		260					265						270		
Pro	Val	Leu	Leu	Asn	Val	Leu	His	Asn	Ile	Ile	Pro	Pro	Ser	Leu	Asn
		275					280					285			
Pro	Thr	Val	Tyr	Ala	Leu	Gln	Thr	Lys	Glu	Leu	Arg	Ala	Ala	Phe	Gln
	290					295					300				
Lys	Val	Leu	Phe	Ala	Leu	Thr	Lys	Glu	Ile	Arg	Ser	Xaa	Arg	Pro	Ser
305					310					315					320
Pro	Xaa	Cys	Thr	Xaa	Thr	Ser	Ala								
				325											

<210> 1362  
 <211> 316  
 <212> PRT  
 <213> Unknown (H38g279 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
 1           5           10           15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
 20           25           30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Ala
 35           40           45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
 50           55           60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65           70           75           80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
 85           90           95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
 100          105          110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115          120          125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
 130          135          140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
 145          150          155          160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
 165          170          175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180          185          190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
 195          200          205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
 210          215          220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225          230          235          240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245          250          255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260          265          270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290          295          300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
 305          310          315

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&lt;210&gt; 1363

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g280 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
 1           5           10           15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
 20           25           30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
 35           40           45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
 50           55           60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

65					70					75					80
Leu	Glu	Cys	Phe	Ala	Gln	Met	Tyr	Ala	Ile	His	Cys	Phe	Val	Ala	Met
				85					90					95	
Glu	Ser	Ser	Thr	Phe	Val	Cys	Met	Ala	Ile	Asp	Arg	Tyr	Val	Ala	Ile
			100					105					110		
Cys	Arg	Pro	Leu	Arg	Tyr	Pro	Ser	Ile	Ile	Thr	Glu	Ser	Phe	Val	Phe
		115					120					125			
Lys	Ala	Asn	Gly	Phe	Met	Ala	Leu	Arg	Asn	Ser	Leu	Cys	Leu	Ile	Ser
	130					135					140				
Val	Pro	Leu	Leu	Ala	Ala	Gln	Arg	His	Tyr	Cys	Ser	Gln	Asn	Gln	Ile
145				150					155					160	
Glu	His	Cys	Leu	Cys	Ser	Asn	Leu	Gly	Val	Thr	Ser	Leu	Ser	Cys	Asp
			165					170						175	
Asp	Arg	Arg	Ile	Asn	Ser	Ile	Asn	Gln	Val	Leu	Leu	Ala	Trp	Thr	Leu
		180					185						190		
Met	Gly	Ser	Asp	Leu	Gly	Leu	Ile	Ile	Leu	Ser	Tyr	Ala	Leu	Ile	Leu
	195					200						205			
Tyr	Ser	Val	Leu	Lys	Leu	Asn	Ser	Pro	Glu	Ala	Ala	Ser	Lys	Ala	Leu
	210					215					220				
Ser	Thr	Cys	Thr	Ser	His	Leu	Ile	Leu	Ile	Leu	Phe	Phe	Tyr	Thr	Val
225					230				235						240
Ile	Ile	Val	Ile	Ser	Ile	Thr	Arg	Ser	Thr	Gly	Met	Arg	Val	Pro	Leu
			245						250					255	
Ile	Pro	Val	Leu	Leu	Asn	Val	Leu	His	Asn	Val	Ile	Pro	Pro	Ala	Leu
		260					265					270			
Asn	Pro	Met	Val	Tyr	Ala	Leu	Lys	Asn	Lys	Glu	Leu	Arg	Gln	Gly	Leu
	275					280						285			
Tyr	Lys	Val	Leu	Arg	Leu	Gly	Val	Lys	Gly	Thr					
	290					295									

&lt;210&gt; 1364

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g281 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1364

Met	Thr	Trp	Ser	Gly	Gly	Thr	Leu	Val	Gly	Glu	Xaa	Gly	Glu	Phe	Val
1				5					10					15	
Leu	Leu	Gly	Phe	Pro	Ala	Pro	Ala	Pro	Leu	Gln	Val	Leu	Ser	Phe	Ala
			20				25					30			
Arg	Xaa	Ser	Ala	Ala	Tyr	Ala	Leu	Val	Leu	Thr	Glu	Asn	Thr	Leu	Ile
	35					40					45				
Ile	Met	Ala	Ser	Arg	Asn	His	Ser	Thr	Leu	His	Lys	Pro	Met	Tyr	Phe
	50				55					60					
Val	Leu	Ala	Asn	Met	Ser	Ser	Leu	Glu	Ile	Trp	Tyr	Val	Thr	Val	Thr
65				70					75					80	
Ile	Pro	Lys	Met	Leu	Ala	Gly	Phe	Val	Gly	Ser	Lys	Gln	Asp	His	Gly
			85						90				95		
Gln	Leu	Ile	Ser	Phe	Glu	Gly	Cys	Met	Thr	Gln	Leu	Tyr	Phe	Phe	Leu
		100				105						110			
Gly	Leu	Gly	Cys	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp
	115					120					125				
Arg	Tyr	Met	Ala	Ile	Cys	Tyr	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Ser
	130					135					140				

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe  
 145 150 155 160  
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys  
 165 170 175  
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu  
 180 185 190  
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile  
 195 200 205  
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser  
 210 215 220  
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly  
 225 230 235 240  
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile  
 245 250 255  
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu  
 260 265 270  
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile  
 275 280 285  
 Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val  
 290 295 300  
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro  
 305 310 315 320  
 Asp Pro Lys Lys Ala Ser Arg  
 325

&lt;210&gt; 1365

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g282 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

<400> 1366																
Met 1	Leu	Leu	Gly	Asn 5	Leu	Ala	Ile	Ile	Ser 10	Phe	Ile	Cys	Leu	Asp 15	Ser	
Arg	Leu	His	Ser 20	Pro	Met	Tyr	Phe	Phe 25	Leu	Cys	Asn	Phe	Ser 30	Leu	Met	
Glu	Met	Val 35	Val	Thr	Ser	Thr	Val 40	Val	His	Arg	Met	Leu 45	Ala	Asp	Leu	
Leu	Ser 50	Thr	His	Lys	Thr	Met 55	Ser	Leu	Ala	Lys	Cys 60	Leu	Thr	Gln	Ser	
Phe 65	Phe	Tyr	Phe	Ser 70	Gly	Ser	Ala	Asn	Phe 75	Leu	Ile	Leu	Met	Val 80		
Met	Ala	Phe	Asp	Arg 85	Tyr	Val	Ala	Ile	Cys 90	His	Pro	Leu	Arg	Tyr 95	Pro	
Thr	Ile	Thr	Asn 100	Gly	Pro	Val	Cys	Val 105	Lys	Leu	Val	Val 110	Ala	Cys	Trp	
Val	Val	Gly 115	Phe	Leu	Ser	Ile	Val 120	Ser	Pro	Thr	Leu	Gln 125	Lys	Thr	Arg	
Leu	Trp 130	Phe	Cys	Gly	Pro	Asn 135	Ile	Ile	Gly	His	Tyr 140	Phe	Cys	Asp	Ser	
Ala 145	Pro	Leu	Leu	Lys 150	Leu	Ala	Cys	Ser	Asp	Thr 155	Arg	His	Ile	Glu	Arg 160	
Met	Asp	Leu	Phe	Leu 165	Ser	Leu	Leu	Phe	Val 170	Leu	Thr	Thr	Met	Leu 175	Leu	
Ile	Ile	Leu	Ser 180	Tyr	Ile	Leu	Ile	Val 185	Ala	Ala	Val	Leu	His 190	Ile	Pro	
Ser	Ser	Ser 195	Gly	Cys	Gln	Lys	Ala 200	Phe	Ser	Thr	Cys	Ala 205	Ser	His	Leu	
Thr	Val 210	Val	Val	Leu	Gly	Tyr 215	Gly	Ser	Ala	Ile	Phe 220	Ile	Tyr	Val	Arg	
Pro 225	Gly	Lys	Gly	His 230	Ser	Thr	Tyr	Leu	Asn	Lys 235	Ala	Val	Ala	Met	Val 240	
Thr	Ala	Met	Val	Thr 245	Pro	Phe	Leu	Asn	Pro 250	Phe	Ile	Phe	Thr	Phe 255	Arg	



Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe  
 260 265 270  
 Leu Gly Asp Pro Ala Ala Cys Arg  
 275 280

<210> 1367

<211> 313

<212> PRT

<213> Unknown (H38g284 protein)

<220>

<223> Synthetic construct

<400> 1367

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
 35 40 45  
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu  
 65 70 75 80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly  
 85 90 95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu  
 130 135 140  
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val  
 145 150 155 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
 180 185 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
 195 200 205  
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
 210 215 220  
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser  
 225 230 235 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
 245 250 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val  
 260 265 270  
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val  
 290 295 300  
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys  
 305 310

<210> 1368

<211> 214

<212> PRT

<213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
          20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
          35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
          50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
          85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
          100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
          115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
          130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
145          150          155          160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
          165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
          180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
          195          200          205
Gly Lys Ile Ser Cys His
          210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
          20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
          35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
          50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
          85           90           95

```

Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys  
 100 105 110  
 Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu  
 115 120 125  
 Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro  
 130 135 140  
 Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu  
 145 150 155 160  
 Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr  
 165 170 175  
 Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His  
 180 185 190  
 Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala  
 195 200 205  
 Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe  
 210 215 220  
 Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala  
 225 230 235 240  
 Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr  
 245 250 255  
 Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met  
 260 265 270  
 Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys  
 275 280 285  
 Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu  
 290 295 300  
 Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys Val  
 305 310 315 320  
 Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile  
 325 330

&lt;210&gt; 1370

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g287 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1370

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe  
 1 5 10 15  
 Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe  
 20 25 30  
 Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val  
 35 40 45  
 Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His  
 50 55 60  
 Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Met Met  
 65 70 75 80  
 Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His  
 85 90 95  
 Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly  
 100 105 110  
 Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr  
 115 120 125  
 Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser  
 130 135 140  
 Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe  
 145 150 155 160  
 Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```

      165      170      175
Arg Gly Gln Leu Leu Lys Leu Ser Cys Asp Asn Thr Leu Leu Thr Glu
      180      185      190
Phe Ile Leu Phe Leu Met Ala Val Phe Ile Leu Ile Gly Ser Leu Ile
      195      200      205
Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr Ile Leu Lys Ile
      210      215      220
Pro Ser Ala Ser Gly Arg Arg Lys Ala Phe Ser Thr Phe Ala Ser His
225      230      235      240
Phe Thr Cys Val Val Ile Gly Tyr Gly Ser Cys Leu Phe Leu Tyr Val
      245      250      255
Lys Pro Lys Gln Thr Gln Gly Val Glu Tyr Asn Lys Ile Val Ser Leu
      260      265      270
Leu Val Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Leu
      275      280      285
Arg Asn Asp Lys Val Lys Glu Ala Leu Arg Asp Gly Met Lys Arg Cys
      290      295      300
Cys Gln Leu Leu Lys Asp
305      310

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&lt;210&gt; 1371

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g288 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1371

```

Met Ser Asn Thr Asn Gly Ser Ala Ile Thr Glu Phe Ile Leu Leu Gly
 1      5      10      15
Leu Thr Asp Cys Pro Glu Leu Gln Ser Leu Leu Phe Val Leu Phe Leu
      20      25      30
Val Val Tyr Leu Val Thr Leu Leu Gly Asn Leu Gly Met Ile Met Leu
      35      40      45
Met Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Asn Ala Thr Pro Gln
      65      70      75      80
Met Ser Thr Asn Ile Val Ser Glu Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Phe Thr Gln Cys Tyr Ile Phe Ile Ala Leu Leu Leu Thr Glu Phe Tyr
      100      105      110
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr Asp Pro
      115      120      125
Leu Arg Tyr Ser Val Lys Thr Ser Arg Arg Val Cys Ile Cys Leu Ala
      130      135      140
Thr Phe Pro Tyr Val Tyr Gly Phe Ser Asp Gly Leu Phe Gln Ala Ile
      145      150      155      160
Leu Thr Phe Arg Leu Thr Phe Cys Arg Ser Ser Val Ile Asn His Phe
      165      170      175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ser Cys Ser Asp Thr Tyr
      180      185      190
Val Lys Glu His Ala Met Phe Ile Ser Ala Gly Phe Asn Leu Ser Ser
      195      200      205
Ser Leu Thr Ile Val Leu Val Ser Tyr Ala Phe Ile Leu Ala Ala Ile
      210      215      220
Leu Arg Ile Lys Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys
      225      230      235      240
Gly Ser His Met Met Ala Val Thr Leu Phe Tyr Gly Thr Leu Phe Cys
      245      250      255

```

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile  
                   260                  265                  270  
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu  
                   290                  295                  300

Arg  
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser  
 1                  5                  10                  15  
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu  
                   20                  25                  30  
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile  
                   35                  40                  45  
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe  
                   50                  55                  60  
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu  
 65                  70                  75                  80  
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met  
                   85                  90                  95  
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile  
                   100                  105                  110  
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu  
                   115                  120                  125  
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly  
                   130                  135                  140  
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser  
 145                  150                  155                  160  
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe  
                   165                  170                  175  
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu  
                   180                  185                  190  
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser  
                   195                  200                  205  
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu  
                   210                  215                  220  
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly  
 225                  230                  235                  240  
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu  
                   245                  250                  255  
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val  
                   260                  265                  270  
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu  
                   275                  280                  285  
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln  
                   290                  295                  300  
 Arg Leu Lys Gly Leu Cys Lys Ala Gln  
 305                  310

<210> 1373

<211> 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g290 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
          20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
          35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
          50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
          85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
          100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
          115          120          125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
          130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145          150          155          160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
          165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
          180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
          195          200          205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
          210          215          220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
225          230          235          240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
          245          250          255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
          260          265          270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
          275          280          285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
          290          295          300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305          310          315

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&lt;210&gt; 1374

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g291 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(345)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1374

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro  
 20 25 30  
 Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu  
 35 40 45  
 Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu  
 65 70 75 80  
 Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser  
 85 90 95  
 Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met  
 100 105 110  
 Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile  
 115 120 125  
 Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu  
 130 135 140  
 Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg  
 145 150 155 160  
 Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu  
 165 170 175  
 Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys  
 180 185 190  
 Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu  
 195 200 205  
 Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala  
 210 215 220  
 Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu  
 225 230 235 240  
 Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys  
 245 250 255  
 Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr  
 260 265 270  
 Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn  
 275 280 285  
 Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp  
 290 295 300  
 Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val  
 305 310 315 320  
 Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln  
 325 330 335  
 Gln Arg Cys Gln Xaa Thr Trp Tyr Lys  
 340 345

&lt;210&gt; 1375

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g292 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(238)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1375

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe  
 1 5 10 15  
 Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

      20      25      30
Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
      35      40      45
Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
      50      55      60
Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
      65      70      75      80
Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
      85      90      95
Leu Pro His Phe Leu Leu Val Asn Phe Phe Phe His Leu Met Arg Leu
      100      105      110
Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
      115      120      125
Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
      130      135      140
Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
      145      150      155      160
Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
      165      170      175
Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
      180      185      190
Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp Ala Ala Glu Xaa Asn
      195      200      205
Lys Val Val Phe Leu Phe Ile Phe Leu Leu Thr Pro Phe Leu Asn Leu
      210      215      220
Leu Thr Gly Gln Ile Tyr Xaa Pro Lys Ser Val Leu Gly Gly
      225      230      235

```

&lt;210&gt; 1376

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g293 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1376

```

Pro Met Lys Val Ala Asn Asn Val Thr Glu Phe Ile Phe Leu Gly Leu
  1      5      10      15
Ser Gln Asp Ser Gly Met Gln Leu Met Phe Phe Val Leu Phe Leu Leu
      20      25      30
Phe Tyr Val Val Ile Met Val Gly Asn Leu Leu Ile Leu Leu Met Val
      35      40      45
Phe Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50      55      60
Leu Ser Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met
      65      70      75      80
Ile Glu Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys
      85      90      95
Ile Thr Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe
      100      105      110
Val Leu Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro
      115      120      125
Leu Arg Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala
      130      135      140
Ser Leu Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu
      145      150      155      160

```



<400> 1377																
Met	Glu	Ile	Leu	Ser	Asn	Ser	Thr	Ser	Lys	Phe	Pro	Thr	Phe	Leu	Leu	
1				5					10					15		
Thr	Gly	Ile	Pro	Gly	Leu	Glu	Ser	Ala	His	Val	Trp	Ile	Ser	Ile	Pro	
			20					25					30			
Phe	Cys	Cys	Phe	Tyr	Ala	Ile	Ala	Leu	Ser	Gly	Asn	Ser	Val	Ile	Leu	
		35					40					45				
Phe	Val	Ile	Ile	Thr	Gln	Gln	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	
	50					55					60					
Leu	Ser	Met	Leu	Ser	Ala	Thr	Asp	Leu	Gly	Leu	Thr	Val	Ser	Ser	Leu	
65					70					75					80	
Ser	Thr	Thr	Leu	Gly	Ile	Leu	Trp	Phe	Glu	Ala	Arg	Glu	Ile	Ser	Leu	
				85					90					95		
Tyr	Ser	Cys	Ile	Val	Gln	Met	Phe	Phe	Leu	His	Gly	Phe	Thr	Phe	Met	
			100					105					110			
Glu	Ser	Gly	Val	Leu	Val	Ala	Thr	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	
		115					120					125				
Cys	Asp	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Asn	Ser	Arg	Ile	Ile	
	130					135					140					
Gln	Met	Gly	Leu	Leu	Met	Ile	Thr	Arg	Ala	Ile	Val	Leu	Ile	Leu	Pro	
145					150					155					160	
Leu	Leu	Leu	Leu	Leu	Lys	Pro	Leu	Tyr	Phe	Cys	Arg	Met	Asn	Ala	Leu	
				165					170					175		
Ser	His	Ser	Tyr	Cys	Tyr	His	Pro	Asp	Val	Ile	Gln	Leu	Ala	Cys	Ser	
			180					185					190			
Asp	Ile	Arg	Ala	Asn	Ser	Ile	Cys	Gly	Leu	Ile	Asp	Leu	Ile	Leu	Thr	
	195						200					205				
Thr	Gly	Ile	Asp	Thr	Pro	Cys	Ile	Val	Leu	Ser	Tyr	Ile	Leu	Ile	Ile	

210	215	220
Arg Phe Val Leu Arg Ile Ala Ser Pro Glu Glu Trp His Lys Val Phe		
225	230	235
Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His		240
	245	250
Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg		255
	260	265
Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val		270
	275	280
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala		285
	290	295
Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp		300
305	310	315
Thr Asn Leu		320

&lt;210&gt; 1378

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g295 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1378

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu	
1	5
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser	10
	20
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser	25
	30
Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe	35
	40
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr	45
65	50
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser	55
	60
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys	65
	70
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala	75
	80
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys	85
	90
Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu	95
145	100
His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile	105
	110
Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser	115
	120
Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe	125
	130
Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile	135
	140
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe	145
225	150
Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr	155
	160
	165
	170
	175
	180
	185
	190
	195
	200
	205
	210
	215
	220
	225
	230
	235
	240
	245
	250
	255

Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pro Pro Arg Asn  
                   260                  265                  270  
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn  
                   275                  280                  285  
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp  
                   290                  295                  300  
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe  
 305                  310                  315                  320  
 Ser

&lt;210&gt; 1379

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g296 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu  
 1                  5                  10                  15  
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro  
                   20                  25                  30  
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe  
                   35                  40                  45  
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe  
 50                  55                  60  
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu  
 65                  70                  75                  80  
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe  
                   85                  90                  95  
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu  
                   100                  105                  110  
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
                   115                  120                  125  
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu  
                   130                  135                  140  
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro  
 145                  150                  155                  160  
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu  
                   165                  170                  175  
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser  
                   180                  185                  190  
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu  
                   195                  200                  205  
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu  
                   210                  215                  220  
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu  
 225                  230                  235                  240  
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro  
                   245                  250                  255  
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg  
                   260                  265                  270  
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val  
                   275                  280                  285  
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala  
                   290                  295                  300  
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg  
 305                  310                  315                  320  
 Gly Leu Arg Gly Arg

325

<210> 1380  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g297 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1380

Met	Glu	Thr	Trp	Val	Asn	Gln	Ser	Tyr	Thr	Asp	Gly	Phe	Phe	Leu	Leu
1				5					10					15	
Gly	Ile	Phe	Ser	His	Ser	Thr	Ala	Asp	Leu	Val	Leu	Phe	Ser	Val	Val
			20					25					30		
Met	Ala	Val	Phe	Thr	Val	Ala	Leu	Cys	Gly	Asn	Val	Leu	Leu	Ile	Phe
		35					40					45			
Leu	Ile	Tyr	Met	Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55				60					
Ser	Gln	Leu	Ser	Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Thr	Asn	Val	Pro
65					70					75					80
Lys	Met	Ala	Ala	Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val
				85					90					95	
Gly	Cys	Gly	Ile	Gln	Ile	Gly	Leu	Phe	Val	Cys	Leu	Val	Gly	Ser	Glu
			100					105					110		
Gly	Leu	Leu	Leu	Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Ser
			115				120						125		
His	Pro	Leu	His	Tyr	Pro	Ile	Leu	Met	Asn	Gln	Arg	Val	Cys	Leu	Gln
	130					135					140				
Ile	Thr	Gly	Ser	Ser	Trp	Ala	Phe	Gly	Ile	Ile	Asp	Gly	Leu	Ile	Gln
145					150					155					160
Met	Val	Val	Val	Met	Asn	Phe	Pro	Tyr	Cys	Gly	Leu	Arg	Lys	Val	Asn
				165					170					175	
His	Phe	Phe	Cys	Glu	Met	Leu	Ser	Leu	Leu	Lys	Leu	Ala	Cys	Val	Asp
			180					185					190		
Thr	Ser	Leu	Phe	Glu	Lys	Val	Ile	Phe	Ala	Cys	Cys	Val	Phe	Met	Leu
		195					200					205			
Leu	Phe	Pro	Phe	Ser	Ile	Ile	Val	Ala	Ser	Tyr	Ala	Arg	Ile	Leu	Gly
	210					215					220				
Thr	Val	Leu	Gln	Met	His	Ser	Ala	Gln	Ala	Trp	Lys	Lys	Ala	Leu	Ala
225					230					235					240
Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Ala	Ala
				245					250					255	
Met	Phe	Ile	Tyr	Leu	Arg	Pro	Arg	His	Tyr	Arg	Ala	Pro	Ser	His	Asp
			260					265					270		
Lys	Val	Ala	Ser	Ile	Phe	Tyr	Thr	Val	Leu	Thr	Pro	Met	Leu	Asn	Pro
		275					280					285			
Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Glu	Val	Met	Gly	Ala	Leu	Arg	Lys
	290					295					300				
Gly	Leu	Asp	Arg	Cys	Arg	Ile	Gly	Ser	Gln	His					
305					310					315					

<210> 1381  
 <211> 323  
 <212> PRT  
 <213> Unknown (H38g298 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1381

```

Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
 1          5          10          15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
      20          25          30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
      35          40          45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
      50          55          60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
 65          70          75          80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
      85          90          95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
      100          105          110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
      115          120          125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
      130          135          140
Ser Lys Ile Ala Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
145          150          155          160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
      165          170          175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
      180          185          190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
      195          200          205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
      210          215          220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
225          230          235          240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
      245          250          255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
      260          265          270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Leu Pro Pro
      275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
      290          295          300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
305          310          315          320
Leu Leu Phe

```

&lt;210&gt; 1382

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g299 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
 1          5          10          15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
      20          25          30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

<210> 1383  
<211> 308  
<212> PRT  
<213> Unknown (H38g300 protein)

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(308)
<223> Xaa = Any Amino Acid
```

<400>: 1383															
Met	Lys	Ile	Asn	Asp	Ser	Ser	Gly	Glu	Asp	Phe	Ile	Leu	Val	Gly	Phe
1				5					10					15	
Ser	Glu	Tyr	Pro	Gln	Ala	Glu	Phe	Ile	Leu	Ser	Leu	Phe	Val	Ser	Gly
			20					25					30		
Phe	Tyr	Thr	Met	Thr	Phe	Thr	Gly	Asn	Thr	Ala	Ile	Ile	Leu	Val	Ser
		35					40					45			
Leu	Leu	Asp	Tyr	Arg	Leu	Arg	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg	Lys
	50					55					60				
Leu	Ser	Phe	Leu	Asp	Met	Cys	Phe	Thr	Thr	Cys	Ile	Val	Leu	Gln	Met
65				70						75				80	
Leu	Val	Asn	Ile	Trp	Gly	Glu	Ser	Lys	Lys	Val	Ser	Tyr	Val	Gly	Cys
				85					90					95	

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val  
 100 105 110  
 Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro  
 115 120 125  
 Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala  
 130 135 140  
 Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser  
 145 150 155 160  
 Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe  
 165 170 175  
 Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly  
 180 185 190  
 Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu  
 195 200 205  
 Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val  
 210 215 220  
 Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe  
 245 250 255  
 Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu  
 260 265 270  
 Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile  
 275 280 285  
 Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile  
 290 295 300  
 Trp Lys Asp Ser  
 305

&lt;210&gt; 1384

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g301 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1384

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu  
 20 25 30  
 Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu  
 35 40 45  
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln  
 65 70 75 80  
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser  
 85 90 95  
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe  
 100 105 110  
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp  
 115 120 125  
 Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu  
 130 135 140  
 Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr  
 145 150 155 160  
 Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His  
 165 170 175  
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```

      180      185      190
Ser Ser Asn Glu Ala Ala Ile Met Val Ser Ser Ile Val Leu Leu Met
      195      200      205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser Thr
      210      215      220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
225      230      235      240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Thr Thr Ile
      245      250      255
Phe Thr Tyr Ile Gln Pro His Ser Gly Pro Ser Val Leu Gln Glu Lys
      260      265      270
Leu Ile Ser Val Phe Tyr Ala Ile Val Met Pro Leu Leu Asn Pro Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp His Lys Leu
      290      295      300
Leu Glu Lys Phe Ser Gly Leu Thr Ser Lys Leu Gly Thr
305      310      315

```

&lt;210&gt; 1385

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g302 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1385

```

Met Glu Gly Lys Asn Gln Thr Asn Ile Ser Glu Phe Leu Leu Leu Gly
 1      5      10      15
Phe Ser Ser Trp Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu
      20      25      30
Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
      35      40      45
Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50      55      60
Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
65      70      75      80
Met Leu Leu Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly
      85      90      95
Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
      100      105      110
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
      130      135      140
Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
145      150      155      160
Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
      165      170      175
Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
      180      185      190
Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
      195      200      205
Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
      210      215      220
Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
225      230      235      240
Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Asn Thr
      245      250      255
Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
      260      265      270

```



Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe  
           275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr  
           290                                  295                                  300  
 Leu Ser  
 305

<210> 1386

<211> 311

<212> PRT

<213> Unknown (H38g303 protein)

<220>

<223> Synthetic construct

<400> 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys  
   1                                  5                                  10                                  15  
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu  
           20                                  25                                  30  
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala  
           35                                  40                                  45  
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe  
           50                                  55                                  60  
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys  
   65                                  70                                  75                                  80  
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly  
           85                                  90                                  95  
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser  
           100                                  105                                  110  
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
           115                                  120                                  125  
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu  
   130                                  135                                  140  
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser  
   145                                  150                                  155                                  160  
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu  
           165                                  170                                  175  
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr  
           180                                  185                                  190  
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala  
           195                                  200                                  205  
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser  
   210                                  215                                  220  
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr  
   225                                  230                                  235                                  240  
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe  
           245                                  250                                  255  
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala  
           260                                  265                                  270  
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe  
           275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu  
           290                                  295                                  300  
 Ile Gly Arg Leu Phe Pro Phe  
 305                                  310

<210> 1387

<211> 313

<212> PRT

<213> Unknown (H38g304 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
          35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
          85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
          100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
          165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
          180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
          195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
          245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
          260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
305          310

```

&lt;210&gt; 1388

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g305 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1388

```

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
          20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
          35           40           45

```

```

Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
          85          90          95
Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
          100          105          110
Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
          130          135          140
Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
145          150          155          160
Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
          165          170          175
Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
          180          185          190
Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
          195          200          205
Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
210          215          220
Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
          245          250          255
Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
          260          265          270
Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
290          295          300
Val Asn Arg Lys Ile Thr Ser Ser Ser
305          310

```

&lt;210&gt; 1389

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g306 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1389

```

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1          5          10          15
Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
          20          25          30
Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
          35          40          45
Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
          50          55          60
Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
65          70          75          80
Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
          85          90          95
Ala Gly

```

&lt;210&gt; 1390

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g307 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1           5           10           15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
          20           25           30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
          35           40           45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
          50           55           60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
65           70           75           80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
          85           90           95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
          100          105          110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
          115          120          125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
130           135           140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
145           150           155           160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
          165          170          175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
          180          185          190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
          195          200          205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
210           215           220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
225           230           235           240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
          245          250          255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
          260          265          270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
          275          280          285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
          290          295          300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
305           310           315           320

```

&lt;210&gt; 1391

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g308 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1391

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
          20           25           30

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser  
 35 40 45  
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu  
 130 135 140  
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His  
 165 170 175  
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr  
 180 185 190  
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile  
 195 200 205  
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr  
 210 215 220  
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile  
 245 250 255  
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr  
 260 265 270  
 Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val  
 290 295 300  
 Val Gly Arg Val Val Phe Ser Val  
 305 310

&lt;210&gt; 1392

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g309 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1392

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr  
 1 5 10 15  
 Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro  
 20 25 30  
 Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile  
 35 40 45  
 Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp  
 50 55 60  
 Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser  
 65 70 75 80  
 Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile  
 85 90 95  
 Ile Thr Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg  
 100 105 110  
 Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

```
<210> 1393
<211> 333
<212> PRT
<213> Unknown (H38g310 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid
```

694

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu  
 305 310 315 320  
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr  
 325 330

&lt;210&gt; 1394

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g311 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu  
 1 5 10 15  
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile  
 20 25 30  
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile  
 35 40 45  
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His  
 50 55 60  
 Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys  
 85 90 95  
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe  
 100 105 110  
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile  
 130 135 140  
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro  
 145 150 155 160  
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe  
 165 170 175  
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala  
 180 185 190  
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile  
 195 200 205  
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val  
 210 215 220  
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr  
 245 250 255  
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val  
 260 265 270  
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu  
 290 295 300  
 Gly Arg Phe Lys Gly Pro Gln

305

310

<210> 1395  
 <211> 295  
 <212> PRT  
 <213> Unknown (H38g312 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(295)  
 <223> Xaa = Any Amino Acid

<400> 1395  
 Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr  
 1 5 10 15  
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu  
 20 25 30  
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile  
 35 40 45  
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu  
 50 55 60  
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu  
 65 70 75 80  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu  
 85 90 95  
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 100 105 110  
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile  
 115 120 125  
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe  
 130 135 140  
 Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr  
 145 150 155 160  
 Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro  
 165 170 175  
 Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu  
 180 185 190  
 Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly  
 195 200 205  
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly  
 210 215 220  
 Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala  
 225 230 235 240  
 Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 245 250 255  
 Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg  
 260 265 270  
 Ile Val Xaa Ser His Phe Leu Ile Cys Ser Ile Pro Ser Val Val  
 275 280 285  
 Xaa Val Arg Lys Gly Ser Lys  
 290 295

<210> 1396  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g313 protein)

<220>  
 <223> Synthetic construct



&lt;400&gt; 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Ser Val Ser Ala Thr
 1          5          10          15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
 20          25          30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
 35          40          45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
 50          55          60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
 65          70          75          80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
 85          90          95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
100          105          110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
115          120          125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
130          135          140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
145          150          155          160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
165          170          175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
180          185          190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
195          200          205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
210          215          220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
225          230          235          240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
245          250          255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
260          265          270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
275          280          285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
290          295          300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305          310

```

&lt;210&gt; 1397

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g314 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1          5          10          15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
 20          25          30
Arg Gln Ser Lys His Pro Ala Leu Leu Cys Val Val Ile Phe Val Val
 35          40          45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
 50          55          60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

```

65          70          75          80
Ser Leu Met Asp Met Ala Tyr Ile Ser Val Thr Val Pro Lys Met Leu
85          90          95
Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro Glu Cys Gly
100        105        110
Met Gln Met Phe Phe Tyr Val Thr Leu Ala Gly Ser Glu Phe Phe Leu
115        120        125
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
130        135        140
Arg Tyr Pro Val Leu Met Asn His Arg Val Cys Leu Phe Leu Ser Ser
145        150        155        160
Gly Cys Trp Phe Leu Gly Ser Val Asp Gly Phe Thr Phe Thr Pro Ile
165        170        175
Thr Met Thr Phe Pro Phe Arg Gly Ser Arg Glu Ile His His Phe Phe
180        185        190
Cys Glu Val Pro Ala Val Leu Asn Leu Ser Cys Ser Asp Thr Ser Leu
195        200        205
Tyr Glu Ile Phe Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile Pro
210        215        220
Val Val Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Ile His
225        230        235        240
Gly Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser
245        250        255
Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Ile Tyr Thr
260        265        270
Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met Val
275        280        285
Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Val Asn Pro Leu Ile Tyr
290        295        300
Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu Thr
305        310        315        320
Val Glu Pro Ala Phe Gln Lys Ala Met Glu
325        330

```

&lt;210&gt; 1398

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g315 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(197)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1398

```

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu
1      5      10      15
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly
20    25    30
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr
35    40    45
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp
50    55    60
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp
65    70    75    80
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu
85    90    95
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr
100   105   110

```

Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His  
           115                          120                          125  
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu  
       130                          135                          140  
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val  
 145                          150                          155                          160  
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
                           165                          170                          175  
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys  
                           180                          185                          190  
 Leu Leu Pro Xaa Gly  
                           195

<210> 1399

<211> 313

<212> PRT

<213> Unknown (H38g316 protein)

<220>

<223> Synthetic construct

<400> 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu  
   1                          5                          10                          15  
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe  
                           20                          25                          30  
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu  
                           35                          40                          45  
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu  
                           50                          55                          60  
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Ser Val Ser Pro  
 65                          70                          75                          80  
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn  
                           85                          90                          95  
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu  
                           100                          105                          110  
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
                           115                          120                          125  
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln  
                           130                          135                          140  
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His  
 145                          150                          155                          160  
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn  
                           165                          170                          175  
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Asn Pro Thr Ile  
                           180                          185                          190  
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala  
                           195                          200                          205  
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile  
                           210                          215                          220  
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser  
 225                          230                          235                          240  
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu  
                           245                          250                          255  
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp  
                           260                          265                          270  
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
                           275                          280                          285  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys  
                           290                          295                          300  
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

&lt;210&gt; 1400

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g317 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1400

```

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1           5           10           15
Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
      20           25           30
Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
      35           40           45
Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
      50           55           60
Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
      65           70           75           80
Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
      85           90           95
Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
      100          105          110
His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
      115          120          125
Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
      130          135          140
Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
      145          150          155          160
Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
      165          170          175
Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
      180          185          190
Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
      195          200          205
Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
      210          215          220
Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
      225          230          235          240
Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
      245          250          255
Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
      260          265          270
Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
      275          280          285
Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
      290          295          300
Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
      305          310          315          320
Gly Ala Gln

```

&lt;210&gt; 1401

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g318 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(128)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1401

```

Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1           5           10           15
Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
      20           25           30
Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
      35           40           45
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
      50           55           60
Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
      65           70           75           80
Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
      85           90           95
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
      100           105           110
Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
      115           120           125

```

&lt;210&gt; 1402

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g319 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1402

```

Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
      20           25           30
Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
      35           40           45
Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
      50           55           60
Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
      65           70           75           80
Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
      85           90           95
Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
      100           105           110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile
      115           120           125
Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
      130           135           140
Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
      145           150           155           160
Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
      165           170           175
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
      180           185           190
Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

```

	195					200				205					
Ser	Asp	Ser	Val	Phe	Ile	Ala	Ile	Ser	Tyr	Met	Leu	Phe	Ile	Leu	Lys
	210					215					220				
Thr	Val	Leu	Gly	Ile	Ala	Ser	His	Gly	Glu	Cys	Leu	Glu	Ala	Leu	Asp
225					230					235					240
Thr	Cys	Val	Ser	His	Ile	Cys	Ala	Val	Leu	Val	Phe	Tyr	Val	Pro	Ile
				245					250					255	
Ile	Thr	Leu	Ala	Thr	Met	Arg	Arg	Phe	Ala	Lys	His	Lys	Ser	Pro	Leu
			260					265					270		
Ala	Met	Ile	Leu	Ile	Ala	Asp	Ala	Phe	Leu	Leu	Val	Pro	Pro	Leu	Met
		275				280						285			
Asn	Pro	Ile	Val	Tyr	Cys	Val	Lys	Thr	Arg	Gln	Ile	Arg	Val	Lys	Val
	290					295					300				
Leu	Glu	Lys	Leu	Ala	Leu	Lys	Pro	Lys	Xaa	Trp	Gly				
305					310					315					

&lt;210&gt; 1403

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g320 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1403

Met	Met	Ala	Ser	Glu	Arg	Asn	Gln	Ser	Ser	Thr	Pro	Thr	Phe	Ile	Leu
1				5				10						15	
Leu	Gly	Phe	Ser	Glu	Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val
			20				25					30			
Phe	Leu	Phe	Val	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile
		35				40					45				
Ile	Ile	Ile	Arg	Leu	Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe
	50				55					60					
Leu	Ser	His	Leu	Ser	Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr
65				70				75						80	
Pro	Lys	Leu	Leu	Glu	Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe
			85					90					95		
Ser	Gly	Cys	Ile	Met	Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr
		100					105					110			
Glu	Thr	Phe	Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val
		115				120						125			
Cys	Lys	Pro	Leu	Leu	Tyr	Thr	Thr	Ile	Met	Ser	Gln	Lys	Leu	Cys	Ala
	130					135					140				
Leu	Leu	Val	Ala	Gly	Ser	Tyr	Thr	Trp	Gly	Ile	Val	Cys	Ser	Leu	Ile
145				150					155					160	
Leu	Thr	Tyr	Phe	Leu	Leu	Asp	Leu	Ser	Phe	Cys	Glu	Ser	Thr	Phe	Ile
			165					170					175		
Asn	Asn	Phe	Ile	Cys	Asp	His	Ser	Val	Ile	Val	Ser	Ala	Ser	Tyr	Ser
		180					185					190			
Asp	Pro	Tyr	Ile	Ser	Gln	Arg	Leu	Cys	Phe	Ile	Ile	Ala	Ile	Phe	Asn
		195				200						205			
Glu	Val	Ser	Ser	Leu	Ile	Ile	Ile	Leu	Thr	Ser	Tyr	Met	Leu	Ile	Phe
	210				215						220				
Thr	Thr	Ile	Met	Lys	Met	Arg	Ser	Ala	Ser	Gly	Arg	Gln	Lys	Thr	Phe
225				230						235					240
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Ile	Phe	His	Gly	Thr
			245					250						255	
Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Pro	Lys	Thr	Ser	Ser	Leu	Ile
		260					265					270			
Val	Thr	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val	Ala	Ile	Pro	Met	Leu	Asn
		275					280					285			

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu  
 290 295 300  
 Lys Leu Val Val Thr Lys Leu Ile Tyr His  
 305 310

<210> 1404

<211> 322

<212> PRT

<213> Unknown (H38g321 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1404

His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr  
 65 70 75 80  
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser  
 305 310 315 320  
 Phe Ser

<210> 1405  
 <211> 330  
 <212> PRT  
 <213> Unknown (H38g322 protein)

<220>  
 <223> Synthetic construct

<400> 1405  
 Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu  
 1 5 10 15  
 Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu  
 35 40 45  
 Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu  
 65 70 75 80  
 Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu  
 85 90 95  
 Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met  
 100 105 110  
 Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala  
 130 135 140  
 Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro  
 145 150 155 160  
 Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu  
 165 170 175  
 Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr  
 180 185 190  
 Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr  
 195 200 205  
 Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile  
 210 215 220  
 Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe  
 225 230 235 240  
 Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro  
 245 250 255  
 Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro  
 260 265 270  
 Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala  
 290 295 300  
 Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu  
 305 310 315 320  
 Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu  
 325 330

<210> 1406  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g323 protein)

<220>  
 <223> Synthetic construct

<400> 1406



```

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1           5           10           15
Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val
 20           25           30
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile
 35           40           45
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
 50           55           60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
 65           70           75           80
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
 85           90           95
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
100           105           110
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
115           120           125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
130           135           140
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
145           150           155           160
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
165           170           175
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
180           185           190
Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn
195           200           205
Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
210           215           220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe
225           230           235           240
Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
245           250           255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
260           265           270
Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
275           280           285
Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
290           295           300
Lys Leu Ile His Thr Gln Val Pro Phe His
305           310

```

&lt;210&gt; 1407

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g324 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1407

```

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile
 1           5           10           15
Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe
 20           25           30
Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu
 35           40           45
Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu
 50           55           60
Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr
 65           70           75           80
Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

```

<400> 1408															
Tyr	Ile	Leu	Leu	Asp	Ile	Tyr	Ile	Cys	Leu	Asn	Asn	Thr	His	Val	Xaa
1				5					10					15	
Leu	Cys	Val	Glu	Ser	Gln	Arg	Gln	Phe	Lys	Ile	Ser	Phe	Tyr	Phe	Ser
			20					25					30		
Phe	Phe	Leu	Leu	Ala	Ile	Thr	Xaa	Phe	Xaa	Xaa	Xaa	Ile	Leu	Ile	Ile
		35					40					45			
Met	Lys	Thr	Xaa	Gln	Tyr	Phe	Leu	Lys	His	Lys	His	Leu	Lys	Lys	Lys
	50					55					60				
Phe	Ser	Xaa	Cys	Leu	Val	Tyr	Ile	Leu	Thr	Tyr	Ile	Leu	Ser	Leu	Xaa
65					70					75					80
Ser	Lys	Phe	Phe	Ala	Leu	Cys	Xaa	Ile	Phe	Ala	Asp	Lys	Ala	Phe	Gln
				85					90					95	
Glu	Gln	Val	Ser	Gly	Asn	Xaa	Xaa	Ser	Arg	Ser	Xaa	Glu	Ser	Pro	Val
			100					105					110		
His	Tyr	Thr	Leu	Thr	Met	Ser	Gln	Lys	Phe	Cys	Ser	Ile	His	Pro	Ala
		115					120					125			
Gly	Cys	Tyr	Asp	Gln	Gly	Ile	Xaa	Ser	Ile	Pro	Gly	His	Ser	Phe	Ser
	130					135					140				

```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
145          150          155          160
Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala
          165          170          175
Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
          180          185          190
Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
          195          200          205
Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
          210          215          220
Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
225          230          235          240
Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
          245          250          255
Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
          260          265          270
Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
          275          280          285

```

&lt;210&gt; 1409

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g326 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1409

```

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu
1      5      10      15
Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu
20     25     30
Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile
35     40     45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
50     55     60
Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65     70     75     80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa
85     90     95
Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile
100    105    110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile
115    120    125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
130    135    140
Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145    150    155    160
His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile
165    170    175
Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser
180    185    190
Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe
195    200    205
Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val
210    215    220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

```

225		230		235		240
Ser Ile Cys Gly	Ser His Leu Ala Val	Val Cys Leu Phe Tyr Gly Thr				
	245	250				
Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Gly Asn		255				
	260	265				
Gly Val Val Ala Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn		270				
	275	280				
Ser Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp		285				
	290	295				
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu		300				
305	310	315				
Phe Leu Cys		320				

&lt;210&gt; 1410

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g327 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1410

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met	
1	5
Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu	
	20
Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile	
	35
Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe	
	50
Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val	
65	70
Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile	
	85
Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly	
	100
Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val	
	115
Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr	
	130
Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro	
145	150
Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn	
	165
Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser	
	180
Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu	
	195
Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn	
	210
Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys	
225	230
Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr	
	245
Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile	
	260
Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met	
	275
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala	
290	295
	300

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln  
 305 310 315

<210> 1411

<211> 312

<212> PRT

<213> Unknown (H38g328 protein)

<220>

<223> Synthetic construct

<400> 1411

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val  
 195 200 205  
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr  
 210 215 220  
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser  
 305 310

<210> 1412

<211> 223

<212> PRT

<213> Unknown (H38g329 protein)

<220>

<223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(223)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1           5           10           15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
          20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
          35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
          50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
          85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Arg Gly Lys Tyr Lys Ala
          115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
          165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
          180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
          195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
          210          215          220

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&lt;210&gt; 1413

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g330 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1413

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
 1           5           10           15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
          20           25           30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
          35           40           45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
          50           55           60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
65           70           75           80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
          85           90           95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
          100          105          110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
          115          120          125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
          130          135          140

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Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val  
 145 150 155 160  
 Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu  
 165 170 175  
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile  
 180 185 190  
 Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys  
 195 200 205  
 Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly  
 210 215 220  
 Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val  
 225 230 235 240  
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile  
 245 250 255  
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg  
 260 265 270  
 Ser Arg Thr Val Glu Ser His Asp  
 275 280

&lt;210&gt; 1414

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g331 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1414

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Gln Ser Gln Asp Ala Gln Leu Leu Val Phe Val Leu Val Leu  
 20 25 30  
 Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr  
 35 40 45  
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg  
 65 70 75 80  
 Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser  
 85 90 95  
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met  
 100 105 110  
 Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu  
 130 135 140  
 Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val  
 145 150 155 160  
 Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn  
 165 170 175  
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr  
 180 185 190  
 Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu  
 195 200 205  
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg  
 210 215 220  
 Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe  
 245 250 255  
 Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln  
 290 295 300  
 His Met Phe Cys  
 305

<210> 1415  
 <211> 154  
 <212> PRT  
 <213> Unknown (H38g332 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(154)  
 <223> Xaa = Any Amino Acid

<400> 1415  
 Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu  
 1 5 10 15  
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser  
 20 25 30  
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Leu Ile  
 35 40 45  
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr  
 50 55 60  
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn  
 65 70 75 80  
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu  
 85 90 95  
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala  
 100 105 110  
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile  
 115 120 125  
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu  
 130 135 140  
 Gly Thr His Gln Val Ser Lys Gln Asn Thr  
 145 150

<210> 1416  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g333 protein)

<220>  
 <223> Synthetic construct

<400> 1416  
 Met Ser Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr  
 1 5 10 15  
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys  
 20 25 30  
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr  
 35 40 45  
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu  
 50 55 60  
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu  
 65 70 75 80



Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Met Leu Val Asn Ile Leu  
                     85                    90                    95  
 Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr  
                     100                    105                    110  
 Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met  
                     115                    120                    125  
 Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His Pro Leu Gln Tyr Pro Ala  
                     130                    135                    140  
 Ile Met Thr Val Arg Phe Cys Gly Lys Leu Val Ser Phe Cys Trp Leu  
 145                    150                    155                    160  
 Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Tyr Ile Ser Gln Leu  
                     165                    170                    175  
 Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp  
                     180                    185                    190  
 Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Cys Ile  
                     195                    200                    205  
 Phe Tyr Thr Gln Ser Ser Leu Val Leu Phe Phe Thr Ser Met Tyr Ile  
                     210                    215                    220  
 Leu Arg Ser Tyr Ile Leu Leu Leu Thr Ala Val Phe Gln Val Pro Ser  
 225                    230                    235                    240  
 Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val  
                     245                    250                    255  
 Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro  
                     260                    265                    270  
 Thr Tyr Gly Ile Pro Thr Leu Leu Gln Lys Ile Leu Thr Leu Val Tyr  
                     275                    280                    285  
 Ser Val Thr Thr Pro Leu Phe Asn Pro Leu Ile Tyr Thr Leu Arg Asn  
                     290                    295                    300  
 Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Phe Gly Met Arg Ile  
 305                    310                    315                    320  
 Arg Gln Asn Ser

&lt;210&gt; 1417

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g334 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1417

Met Ala Asn Ile Thr Arg Met Ala Asn His Thr Gly Lys Leu Asp Phe  
 1                    5                    10                    15  
 Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser  
                     20                    25                    30  
 Val Val Ile Phe Val Val Phe Leu Lys Ala Leu Ser Gly Asn Ala Val  
                     35                    40                    45  
 Leu Ile Leu Leu Ile His Cys Asp Ala His Leu His Ser Pro Met Tyr  
                     50                    55                    60  
 Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val  
 65                    70                    75                    80  
 Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Val  
                     85                    90                    95  
 Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala  
                     100                    105                    110  
 Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val  
                     115                    120                    125  
 Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val  
                     130                    135                    140  
 Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp Gly

145		150		155		160
Phe Met Leu Thr	Pro Ile Thr Met Ser	Phe Pro Phe Cys Arg Ser Trp				
	165	170				
Glu Ile His His	Phe Phe Cys Glu Val	Pro Ala Val Thr Ile Leu Ser				
	180	185				
Cys Ser Asp Thr	Ser Leu Tyr Glu Thr	Leu Met Tyr Leu Cys Cys Val				
	195	200				
Leu Met Leu Leu	Ile Pro Val Thr	Ile Ile Ser Ser Ser Tyr Leu Leu				
	210	215				
Ile Leu Leu Thr	Val His Arg Met Asn Ser	Ala Glu Gly Arg Lys Lys				
	225	230				
Ala Phe Ala Thr	Cys Ser Ser His Leu Thr	Val Val Ile Leu Phe Tyr				
	245	250				
Gly Ala Ala Val	Tyr Thr Tyr Met Leu	Pro Ser Ser Tyr His Thr Pro				
	260	265				
Glu Lys Asp Met	Met Val Ser Val	Phe Tyr Thr Ile Leu Thr Pro Val				
	275	280				
Leu Asn Pro Leu	Ile Tyr Ser Leu Arg	Asn Lys Asp Val Met Gly Ala				
	290	295				
Leu Lys Lys Met	Leu Thr Val Arg	Phe Val Leu				
305	310	315				

&lt;210&gt; 1418

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g335 protein)

&lt;220&gt; .

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(253)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1418

Ser His Leu Ser	Val Ile Asp Thr	Leu Tyr Ile Ser	Thr Ile Val Pro
1	5	10	15
Lys Met Leu Val	Asp Tyr Leu Met	Gly Glu Gly Thr	Ile Ser Phe Ile
	20	25	30
Ala Cys Thr Ala	Gln Cys Phe Leu	Tyr Met Gly Phe	Met Gly Ala Glu
	35	40	45
Phe Phe Leu Leu	Gly Leu Met Ala	Tyr Asp Arg Tyr	Val Ala Ile Cys
	50	55	60
Asn Pro Leu Arg	Tyr Pro Val Leu	Ile Ser Trp Arg	Val Cys Trp Met
	65	70	75
Ile Leu Ala Ser	Ser Trp Phe Gly	Gly Ala Leu Asp	Ser Phe Leu Leu
	85	90	95
Thr Pro Ile Thr	Met Ser Leu Pro	Phe Cys Ala Ser	His Gln Ile Asn
	100	105	110
His Phe Phe Cys	Glu Ala Pro Thr	Met Leu Arg Leu	Ala Cys Gly Asp
	115	120	125
Lys Thr Thr Tyr	Glu Thr Val Met	Tyr Val Cys Cys	Val Ala Met Leu
	130	135	140
Leu Ile Pro Phe	Ser Val Val Thr	Ala Ser Tyr Thr	Arg Ile Leu Ile
	145	150	155
Thr Val His Gln	Met Thr Ser Ala	Glu Gly Arg Lys	Lys Ala Phe Ala
	165	170	175
Thr Cys Ser Ser	His Met Met Val	Val Thr Leu Phe	Tyr Gly Ala Ala
	180	185	190
Leu Tyr Thr Tyr	Thr Leu Pro Gln	Ser Tyr His Thr	Pro Ile Lys Asp
	195	200	205

Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro  
 210 215 220  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg  
 225 230 235 240  
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg  
 245 250

<210> 1419  
 <211> 285  
 <212> PRT  
 <213> Unknown (H38g336 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(285)  
 <223> Xaa = Any Amino Acid

<400> 1419  
 Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp  
 1 5 10 15  
 Leu Thr Pro Val Phe Phe Leu Ser Pro Ser Cys Pro Ser Pro Ile Ala  
 20 25 30  
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg  
 35 40 45  
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly  
 50 55 60  
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala  
 65 70 75 80  
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys  
 85 90 95  
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe  
 100 105 110  
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu  
 115 120 125  
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys  
 130 135 140  
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile  
 145 150 155 160  
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val  
 165 170 175  
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala  
 180 185 190  
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala  
 195 200 205  
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser  
 210 215 220  
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu  
 225 230 235 240  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val  
 245 250 255  
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg  
 260 265 270  
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys  
 275 280 285

<210> 1420  
 <211> 271  
 <212> PRT  
 <213> Unknown (H38g337 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(271)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10           15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
 20           25           30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
 35           40           45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
 50           55           60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
 65           70           75           80
Leu Tyr Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
 85           90           95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
 100          105          110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
 115          120          125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
 130          135          140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
 145          150          155          160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
 165          170          175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
 180          185          190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
 195          200          205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
 210          215          220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
 225          230          235          240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
 245          250          255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
 260          265          270

```

&lt;210&gt; 1421

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g338 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10           15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
 20           25           30

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile  
 35 40 45  
 Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe  
 50 55 60  
 Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr  
 65 70 75 80  
 Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe  
 85 90 95  
 Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala  
 100 105 110  
 Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala  
 130 135 140  
 Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr  
 145 150 155 160  
 Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile  
 165 170 175  
 Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser  
 180 185 190  
 Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn  
 195 200 205  
 Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe  
 210 215 220  
 Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
 245 250 255  
 Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile  
 260 265 270  
 Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn  
 275 280 285  
 Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu  
 290 295 300  
 Ser Xaa Xaa Ile Thr Gln  
 305 310

&lt;210&gt; 1422

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g339 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(217)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1422

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met  
 1 5 10 15  
 Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val  
 20 25 30  
 Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe  
 35 40 45  
 Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe  
 50 55 60  
 Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser  
 65 70 75 80  
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

```
<210> 1423
<211> 311
<212> PRT
<213> Unknown (H38g340 protein)
```

<400> 1423

718

Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val  
 290 295 300  
 Met Gly Ser Lys Ile His Ser  
 305 310

<210> 1424

<211> 321

<212> PRT

<213> Unknown (H38g341 protein)

<220>

<223> Synthetic construct

<400> 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu  
 1 5 10 15  
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val  
 20 25 30  
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile  
 35 40 45  
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala  
 65 70 75 80  
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe  
 85 90 95  
 Ser Gly Cys Leu Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr  
 100 105 110  
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala  
 130 135 140  
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr  
 145 150 155 160  
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile  
 165 170 175  
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro  
 180 185 190  
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn  
 195 200 205  
 Glu Ile Ser Thr Leu Leu Ile Leu Thr Ser Tyr Ala Phe Ile Ile  
 210 215 220  
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe  
 225 230 235 240  
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
 245 250 255  
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr  
 260 265 270  
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn  
 275 280 285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg  
 290 295 300  
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr  
 305 310 315 320  
 Pro

<210> 1425

<211> 101

<212> PRT  
 <213> Unknown (H38g342 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(101)  
 <223> Xaa = Any Amino Acid

<400> 1425  
 Cys Cys Pro Leu His His His Tyr Leu Pro Arg Gln Ser Leu Asp Gln  
 1 5 10 15  
 Leu Thr Tyr Leu Ile Ala Leu Ile Phe Asn Phe Leu Phe Val Phe Gly  
 20 25 30  
 Leu Gln Ser Ser Phe Ile Phe Leu Lys Ala Xaa Gln Cys Phe Pro Lys  
 35 40 45  
 Asp Ile His Tyr Ile Phe Val Lys Ala Arg Arg Ala Ser Gly Tyr Leu  
 50 55 60  
 Thr Tyr His Ile Ala Gly Asn Arg Ser Xaa Thr Val Phe Phe Leu Val  
 65 70 75 80  
 Cys Asn Cys His Tyr Tyr Gly Asp Asp Ile Gly Xaa Val Xaa Ile Phe  
 85 90 95  
 Tyr Val Asn Ile Leu  
 100

<210> 1426  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g343 protein)

<220>  
 <223> Synthetic construct

<400> 1426  
 Met Pro Val Gly Lys Leu Val Phe Asn Gln Ser Glu Pro Thr Glu Phe  
 1 5 10 15  
 Val Phe Arg Ala Phe Thr Thr Ala Thr Glu Phe Gln Val Leu Leu Phe  
 20 25 30  
 Leu Leu Phe Leu Leu Leu Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala  
 35 40 45  
 Ile Ile Trp Val Val Cys Thr His Ser Thr Leu Arg Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Ser Asn Leu Ser Phe Leu Glu Leu Cys Tyr Thr Thr Val  
 65 70 75 80  
 Val Val Pro Leu Met Leu Ser Asn Ile Leu Gly Ala Gln Lys Pro Ile  
 85 90 95  
 Ser Leu Ala Gly Cys Gly Ala Gln Met Phe Phe Phe Val Thr Leu Gly  
 100 105 110  
 Ser Thr Asp Cys Phe Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu His Tyr Thr Leu Ile Met Thr Arg Glu Leu  
 130 135 140  
 Cys Thr Gln Met Leu Gly Gly Ala Leu Gly Leu Ala Leu Phe Pro Ser  
 145 150 155 160  
 Leu Gln Leu Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly His His  
 165 170 175  
 Gln Glu Ile Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu  
 180 185 190  
 Ala Cys Ala Asp Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser  
 195 200 205



Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val  
 210 215 220  
 Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg  
 225 230 235 240  
 Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln  
 245 250 255  
 Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser  
 260 265 270  
 Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro  
 275 280 285  
 Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly  
 290 295 300  
 Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn  
 305 310 315

&lt;210&gt; 1427

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g344 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(208)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1427

Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe  
 20 25 30  
 Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu  
 35 40 45  
 Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys  
 65 70 75 80  
 Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly  
 85 90 95  
 Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu  
 130 135 140  
 Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr  
 145 150 155 160  
 Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe  
 165 170 175  
 Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr  
 180 185 190  
 Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile  
 195 200 205

&lt;210&gt; 1428

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g345 protein)

&lt;220&gt;

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Pro Gly Leu Ser
 20           25           30
Leu Ser Met Tyr Leu Leu Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser Asn Pro Ser Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser
 85           90           95
Cys Leu Thr Gln Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp
 100          105          110
Met Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115          120          125
Ser Pro His Tyr Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe
 130          135          140
Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145          150          155          160
Trp Thr Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180          185          190
Val Ile Asp Ser Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe
 195          200          205
Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser
 210          215          220
Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr
 225          230          235          240
Cys Arg Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245          250          255
Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Gly Asp Gly Val
 260          265          270
Val Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Cys Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290          295          300
Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305          310          315          320
Cys

```

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

&lt;400&gt; 1429

```

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1           5           10           15
Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
 20           25           30
Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
 35           40           45
Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
 50           55           60
Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
 65           70           75           80
Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
 85           90           95
Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
100           105           110
Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
115           120           125
Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
130           135           140
Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
145           150           155           160
Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
165           170           175
Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
180           185           190
Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met
195           200           205
Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
210           215           220
Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
225           230           235           240
Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
245           250           255
Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
260           265           270
Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
275           280           285
Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
290           295           300
Ile Gly Asn Phe Trp Val
305           310

```

&lt;210&gt; 1430

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g347 protein)

&lt;220&gt;.

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1430

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe
 20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu

```

35	40	45																	
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu																			
50	55	60																	
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala																			
65	70	75																	
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala																			
85	90	95																	
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu																			
100	105	110																	
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile																			
115	120	125																	
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly																			
130	135	140																	
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala																			
145	150	155																	
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val																			
165	170	175																	
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala																			
180	185	190																	
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala																			
195	200	205																	
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys																			
210	215	220																	
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa																			
225	230	235																	
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr																			
245	250	255																	
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro																			
260	265	270																	
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met																			
275	280	285																	
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val																			
290	295	300																	
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile																			
305	310	315																	
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys																			
325	330	335																	

&lt;210&gt; 1431

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g348 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1431

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln																			
1	5	10																	
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys																			
20	25	30																	
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr																			
35	40	45																	
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu																			
50	55	60																	
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser																			
65	70	75																	
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val																			
85	90	95																	
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr																			
100	105	110																	

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu  
 115 120 125  
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn  
 130 135 140  
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile  
 145 150 155 160  
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu  
 165 170 175  
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys  
 180 185 190  
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn  
 195 200 205  
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe  
 210 215 220  
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg  
 225 230 235 240  
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser  
 245 250 255  
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr  
 260 265 270  
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala  
 275 280 285  
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser  
 290 295 300  
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg  
 305 310 315 320  
 Lys Ile Ser Ser Leu  
 325

&lt;210&gt; 1432

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g349 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser  
 1 5 10 15  
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg  
 20 25 30  
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala  
 35 40 45  
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu  
 50 55 60  
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro  
 65 70 75 80  
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu  
 85 90 95  
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly  
 100 105 110  
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser  
 115 120 125  
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile  
 130 135 140  
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr  
 145 150 155 160  
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro  
 165 170 175  
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

180 185 190  
 Phe His Gly Val Ile Leu Leu Leu Tyr Cys Val Pro Asn Ser Lys Ser  
 195 200 205  
 Ser Trp Leu Leu Val Lys Val Ala Thr Val Leu Phe Thr Val Ile Ile  
 210 215 220  
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 225 230 235 240  
 Gly Thr Val Arg Lys Leu Ile Asn Ser Gln Ser Pro Phe His Ser Lys  
 245 250 255

&lt;210&gt; 1433

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g350 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1433

Met Ala Glu Ser Gly Thr Thr Val Thr Glu Phe Phe Leu Arg Gly Phe  
 1 5 10 15  
 Arg Leu Lys Ala Glu Leu Gln Ile Gly Leu Phe Phe Val Phe Leu Val  
 20 25 30  
 Ile Phe Leu Ile Thr Met Gly Gly Asn Leu Gly Met Ile Val Leu Met  
 35 40 45  
 Leu Ile Gln Thr Asp Pro Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser His Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Ile Gly Pro  
 65 70 75 80  
 Gln Leu Leu Glu Thr Leu Ala Thr Asp Lys Met Ile Ile Thr Tyr Glu  
 85 90 95  
 Arg Cys Ala Ser Gln Phe Phe Phe Phe Thr Leu Cys Ala Ser Ile Glu  
 100 105 110  
 Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Ala Ile Val Met Thr Pro Lys Thr Arg Leu Ala  
 130 135 140  
 Leu Leu Ala Gly Ala Tyr Ser Gly Ala Ile Val Asn Ser Val Ile Cys  
 145 150 155 160  
 Thr Gly Cys Thr Phe Ser Ile Ser Phe Ser Lys Ser Asn His Val Asp  
 165 170 175  
 Phe Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Glu  
 180 185 190  
 Thr Arg Pro Arg Glu Trp Val Ile Tyr Leu Ser Ala Phe Leu Val Ile  
 195 200 205  
 Thr Thr Ser Ile Ser Val Ile Leu Thr Ser Tyr Leu Phe Ile Ile Gln  
 210 215 220  
 Ser Val Leu Lys Ile Arg Thr Ala Gly Gly Arg Ala Lys Thr Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Met Thr Ala Leu Thr Leu Phe Phe Gly Thr Leu  
 245 250 255  
 Ile Phe Ile Tyr Leu Lys Gly Asn Met Gly Glu Ser Leu Glu Glu Asp  
 260 265 270  
 Lys Ile Val Ser Ile Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Met Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys  
 290 295 300

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu  
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe  
 20 25 30  
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val  
 35 40 45  
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu  
 100 105 110  
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu  
 130 135 140  
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu  
 145 150 155 160  
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn  
 165 170 175  
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp  
 180 185 190  
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu  
 195 200 205  
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val  
 210 215 220  
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile  
 245 250 255  
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val  
 260 265 270  
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu  
 290 295 300  
 Ile Leu Asp Thr Lys Val Phe Ser Tyr  
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
 1           5           10           15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu
           20           25           30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
           35           40           45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
           50           55           60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
65           70           75           80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
           85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
           100          105          110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
           115          120          125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
           130          135          140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
145           150          155          160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
           165          170          175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
           180          185          190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
           195          200          205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
210          215          220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
           245          250          255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
           260          265          270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
           275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
290          295          300
Leu Ser Lys Ser Lys Pro Ala Arg
305          310

```

&lt;210&gt; 1436

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g353 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
 1           5           10           15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
           20           25           30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
           35           40           45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
           50           55           60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
65           70           75           80

```



Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu  
 85 90 95  
 Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His  
 100 105 110  
 Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys  
 115 120 125  
 Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala  
 130 135 140  
 Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr  
 145 150 155 160  
 Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg  
 165 170 175  
 Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile  
 180 185 190  
 Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys  
 195 200 205  
 Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu  
 210 215 220  
 Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln  
 225 230 235 240  
 Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr  
 245 250

<210> 1437  
 <211> 188  
 <212> PRT  
 <213> Unknown (H38g354 protein)

<220>  
 <223> Synthetic construct

<400> 1437

Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly  
 1 5 10 15  
 Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu  
 20 25 30  
 Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu  
 35 40 45  
 Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly  
 85 90 95  
 Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys  
 100 105 110  
 Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu  
 130 135 140  
 Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met  
 145 150 155 160  
 Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Ser  
 180 185

<210> 1438  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g355 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1438

Leu	Asn	Phe	Ile	Ile	Phe	Phe	Arg	Xaa	Thr	Ser	Tyr	Ile	Glu	Pro	Met
1				5					10					15	
Ala	Lys	Arg	Asn	Leu	Ser	Thr	Val	Thr	Glu	Phe	Ile	Leu	Val	Val	Phe
			20					25					30		
Thr	Asp	His	Pro	Glu	Leu	Ala	Val	Pro	Leu	Phe	Leu	Val	Phe	Leu	Ser
		35					40					45			
Phe	Tyr	Leu	Val	Thr	Phe	Leu	Gly	Asn	Gly	Gly	Met	Ile	Ile	Leu	Ile
50						55					60				
Gln	Val	Asp	Ala	Gln	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu	Ser	His
65					70					75					80
Leu	Ala	Phe	Leu	Asp	Ala	Cys	Cys	Ala	Ser	Val	Ile	Thr	Pro	Gln	Ile
				85				90						95	
Leu	Ala	Thr	Leu	Ala	Thr	Asp	Lys	Thr	Val	Ile	Ser	Tyr	Gly	Cys	Arg
			100					105					110		
Ala	Val	Gln	Phe	Ser	Phe	Phe	Thr	Ile	Cys	Ala	Gly	Thr	Glu	Cys	Tyr
		115					120					125			
Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Ser	Asn	Pro
130						135					140				
Leu	His	Cys	Asn	Met	Thr	Met	Thr	Pro	Gly	Thr	Cys	Arg	Val	Phe	Leu
145				150						155					160
Ala	Ser	Ala	Phe	Ile	Cys	Gly	Val	Ser	Gly	Ala	Ile	Leu	His	Thr	Thr
			165					170					175		
Cys	Thr	Phe	Thr	Leu	Ser	Phe	Cys	Cys	Asp	Asn	Gln	Ile	Asn	Phe	Phe
			180					185					190		
Phe	Cys	Asp	Leu	Pro	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Ser	Met	Thr
		195					200					205			
Gln	Thr	Glu	Ile	Val	Ile	Leu	Leu	Cys	Ala	Lys	Cys	Met	Phe	Leu	Ala
210						215					220				
Asn	Val	Met	Val	Ile	Leu	Ile	Cys	Tyr	Met	Leu	Ile	Ile	Arg	Ala	Ile
225					230					235					240
Leu	Arg	Val	Lys	Ser	Ala	Gly	Gly	Xaa	Ala	Lys	Thr	Phe	Ser	Thr	Cys
			245					250						255	
Thr	Ser	His	Leu	Thr	Thr	Val	Val	Leu	Phe	Phe	Gly	Thr	Leu	Ala	Phe
			260					265					270		
Met	Tyr	Gln	Arg	Ser	Asn	Ser	Ala	Lys	Ser	Ser	Glu	Glu	Asp	Lys	Ile
		275					280					285			
Val	Ser	Val	Phe	Tyr	Thr	Val	Ile	Ile	Pro	Met	Leu	Asn	Pro	Leu	Ile
		290				295					300				
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Ala	Ala	Phe	Gly	Lys	Leu	Val
305					310					315					320
Gly	Lys	Phe	Gln	Phe	Pro										
				325											

&lt;210&gt; 1439

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g356 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1439

```

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1           5           10           15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
          20           25           30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
          35           40           45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
          50           55           60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
          65           70           75           80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
          85           90           95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
          100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
          115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
          130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
          145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
          165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
          180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
          195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
          210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
          225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
          245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
          260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
          275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
          290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
          305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
          325

```

&lt;210&gt; 1440

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g357 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
          20           25           30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

```

```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
  50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
  65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
      145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
      290      295      300
Met Gly Ser Lys Ile His Ser
      305      310

```

&lt;210&gt; 1441

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g358 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(209)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1441

```

Cys His Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
  1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
      50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
      65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr  
                   100                  105                  110  
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe  
                   115                  120                  125  
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser  
                   130                  135                  140  
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro  
                   145                  150                  155                  160  
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser  
                   165                  170                  175  
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu  
                   180                  185                  190  
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val  
                   195                  200                  205  
 Lys

&lt;210&gt; 1442

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g359 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe  
   1                  5                  10                  15  
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp  
                   20                  25                  30  
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile  
                   35                  40                  45  
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser  
                   50                  55                  60  
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu  
   65                  70                  75                  80  
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu  
                   85                  90                  95  
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu  
                   100                  105                  110  
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala  
                   115                  120                  125  
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro  
                   130                  135                  140  
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser  
   145                  150                  155                  160  
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr  
                   165                  170                  175  
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser  
                   180                  185                  190  
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys  
                   195                  200                  205  
 Ala Lys Leu Phe  
                   210

&lt;210&gt; 1443

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g360 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1           5           10           15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
          20           25           30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
          35           40           45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
          50           55           60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65          70           75           80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
          85           90           95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
          100          105          110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
          115          120          125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
          130          135          140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
          145          150          155          160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
          165          170          175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
          180          185          190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
          195          200          205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
          210          215          220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
          225          230          235          240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
          245          250          255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
          260          265          270
Val Val Met Gly Asp Ile Tyr Leu Leu Pro Pro Val Ile Asn Pro
          275          280          285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
          290          295          300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
          305          310          315

```

&lt;210&gt; 1444

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g361 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1           5           10           15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
          20           25           30

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met  
 35 40 45  
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys  
 50 55 60  
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala  
 65 70 75 80  
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro  
 85 90 95  
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly  
 100 105 110  
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe  
 115 120 125  
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser  
 130 135 140  
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg  
 145 150 155 160  
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val  
 165 170 175  
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val  
 180 185 190  
 Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys  
 195 200 205  
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly  
 210 215 220  
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val  
 225 230 235 240  
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu  
 245 250 255  
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met  
 260 265 270  
 Phe Ser Gln Gly Gly Lys  
 275

&lt;210&gt; 1445

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g362 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1445

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

145		150		155		160									
Thr	Pro	Leu	Ser	Trp	Met	Met	Asn	His	Leu	Pro	Phe	Cys	Gly	Ser	Asn
				165					170					175	
Val	Val	Val	His	Ser	Tyr	Cys	Lys	His	Ile	Ala	Leu	Ala	Arg	Leu	Ala
			180					185					190		
Cys	Ala	Asp	Pro	Val	Pro	Ser	Ser	Leu	Tyr	Ser	Leu	Ile	Gly	Ser	Ser
		195				200						205			
Leu	Met	Val	Gly	Ser	Asp	Val	Ala	Phe	Ile	Ala	Ala	Ser	Tyr	Ile	Leu
	210				215						220				
Ile	Leu	Arg	Ala	Val	Phe	Asp	Leu	Ser	Ser	Lys	Thr	Ala	Gln	Leu	Lys
225				230						235				240	
Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Val	Gly	Val	Met	Ala	Leu	Tyr	Tyr
			245					250					255		
Leu	Pro	Gly	Met	Ala	Ser	Ile	Tyr	Ala	Ala	Trp	Leu	Gly	Gln	Asp	Ile
		260					265						270		
Val	Pro	Leu	His	Thr	Gln	Val	Leu	Ala	Ala	Asp	Leu	Tyr	Val	Ile	Ile
		275				280						285			
Pro	Ala	Thr	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Met	Arg	Thr	Lys	Gln	Leu
	290					295					300				
Leu	Glu	Gly	Ile	Trp	Ser	Tyr	Leu	Met	His	Phe	Leu	Phe	Asp	His	
305					310					315					

&lt;210&gt; 1446

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g363 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1446

Met	Asn	Glu	Thr	Asn	His	Ser	Trp	Val	Thr	Glu	Phe	Val	Leu	Leu	Gly
1				5				10					15		
Leu	Ser	Ser	Ser	Arg	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Leu	Ile	Phe	Ser
			20				25						30		
Leu	Leu	Tyr	Leu	Ala	Ile	Leu	Leu	Gly	Asn	Phe	Leu	Ile	Ile	Leu	Thr
		35				40						45			
Val	Thr	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Phe	Ile	Asp	Val	Cys	Val	Ala	Ser	Ser	Ala	Thr	Pro	Lys
65				70						75				80	
Met	Ile	Ala	Asp	Phe	Leu	Val	Glu	His	Lys	Thr	Ile	Ser	Phe	Asp	Ala
			85					90					95		
His	Leu	Ala	Gln	Ile	Phe	Phe	Val	His	Leu	Phe	Thr	Gly	Ser	Glu	Met
		100					105					110			
Val	Leu	Leu	Val	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys
		115				120						125			
Pro	Pro	His	Tyr	Met	Thr	Ile	Met	Ser	Cys	Cys	Val	Cys	Val	Val	Leu
	130				135						140				
Val	Leu	Ile	Ser	Trp	Phe	Val	Gly	Phe	Ile	His	Thr	Thr	Ser	Gln	Leu
145				150						155				160	
Ala	Phe	Thr	Val	Asn	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Lys	Val	Asp	Ser
			165						170					175	
Phe	Phe	Cys	Asp	Leu	Pro	Leu	Ala	Thr	Lys	Leu	Ala	Cys	Ile	Asp	Thr
		180					185						190		
Tyr	Val	Val	Ser	Leu	Leu	Ile	Val	Ala	Asp	Ser	Gly	Phe	Leu	Ser	Leu
		195				200						205			
Ser	Ser	Phe	Leu	Leu	Leu	Val	Val	Ser	Tyr	Thr	Val	Ile	Leu	Val	Thr
	210					215					220				
Val	Arg	Asn	Arg	Ser	Ser	Val	Ser	Met	Val	Lys	Ala	His	Ser	Thr	Leu
225					230					235					240



Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Ser Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg  
 290 295 300  
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe  
 305 310 315 320  
 Leu Glu

&lt;210&gt; 1447

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g364 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1447

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
 145 150 155 160  
 Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
 180 185 190  
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
 195 200 205  
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
 210 215 220  
 Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
 245 250 255  
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val  
 260 265 270  
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
 275 280 285  
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
 290 295 300  
 Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser

305  
Asn Leu

310

315

320

<210> 1448  
<211> 314  
<212> PRT  
<213> Unknown (H38g365 protein)

<220>  
<223> Synthetic construct

<400> 1448  
Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
1 5 10 15  
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser  
20 25 30  
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
35 40 45  
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser  
50 55 60  
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met  
65 70 75 80  
Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys  
85 90 95  
Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val  
100 105 110  
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro  
115 120 125  
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val  
130 135 140  
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu  
145 150 155 160  
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser  
165 170 175  
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile  
180 185 190  
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu  
195 200 205  
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile  
210 215 220  
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys  
225 230 235 240  
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe  
245 250 255  
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser  
260 265 270  
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr  
275 280 285  
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile  
290 295 300  
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro  
305 310

<210> 1449  
<211> 317  
<212> PRT  
<213> Unknown (H38g366 protein)

<220>  
<223> Synthetic construct

<400> 1449  
 Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
 65 70 75 80  
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
 85 90 95  
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
 100 105 110  
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
 130 135 140  
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
 145 150 155 160  
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
 180 185 190  
 Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu  
 195 200 205  
 Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile  
 210 215 220  
 Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr  
 225 230 235 240  
 Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val  
 245 250 255  
 Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro  
 260 265 270  
 Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro  
 275 280 285  
 Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu  
 290 295 300  
 Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg  
 305 310 315

<210> 1450

<211> 101

<212> PRT

<213> Unknown (H38g367 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1450

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val  
 1 5 10 15  
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr  
 20 25 30  
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```

      35              40              45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50              55              60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
  65              70              75              80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
      85              90              95
Cys Cys Leu Ala Glu
      100

```

<210> 1451  
 <211> 169  
 <212> PRT  
 <213> Unknown (H38g368 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(169)  
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1              5              10              15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
      20              25              30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
      35              40              45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
      50              55              60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
      65              70              75              80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
      85              90              95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
      100              105              110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
      115              120              125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
      130              135              140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
      145              150              155              160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
      165

```

<210> 1452  
 <211> 279  
 <212> PRT  
 <213> Unknown (H38g369 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(279)  
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1              5              10              15

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys  
                   20                  25                  30  
 Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser  
                   35                  40                  45  
 Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met  
                   50                  55                  60  
 Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu  
 65                  70                  75                  80  
 Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp  
                   85                  90                  95  
 Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile  
                   100                  105                  110  
 Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe  
                   115                  120                  125  
 Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val  
 130                  135                  140  
 Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala  
 145                  150                  155                  160  
 His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa  
                   165                  170                  175  
 Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys  
                   180                  185                  190  
 Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu  
                   195                  200                  205  
 Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu  
                   210                  215                  220  
 Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr  
 225                  230                  235                  240  
 Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe  
                   245                  250                  255  
 Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu  
                   260                  265                  270  
 Ser Ile Ile Leu Thr Leu Val  
                   275

&lt;210&gt; 1453

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g370 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(154)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1453

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile  
   1                  5                  10                  15  
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe  
                   20                  25                  30  
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg  
                   35                  40                  45  
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys  
                   50                  55                  60  
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile  
 65                  70                  75                  80  
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu  
                   85                  90                  95  
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

```

          100          105          110
Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
          115          120          125
Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
          130          135          140
Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
145          150

```

<210> 1454  
 <211> 186  
 <212> PRT  
 <213> Unknown (H38g371 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(186)  
 <223> Xaa = Any Amino Acid

```

<400> 1454
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
1      5      10      15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
          20      25      30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Thr Pro Asn Ile Phe
          35      40      45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
50      55      60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
65      70      75      80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
          85      90      95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
          100      105      110
Arg Ser His Ser Leu Gln His Ala Val Ala Ser Pro Cys Pro Gly
          115      120      125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
130      135      140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145      150      155      160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
          165      170      175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
          180      185

```

<210> 1455  
 <211> 142  
 <212> PRT  
 <213> Unknown (H38g372 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(142)  
 <223> Xaa = Any Amino Acid

```

<400> 1455
Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
1      5      10      15

```

Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys  
                   20                  25                  30  
 Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile  
           35                  40                  45  
 Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys  
           50                  55                  60  
 Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe  
   65                  70                  75                  80  
 Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu  
                   85                  90                  95  
 Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met  
                   100                  105                  110  
 Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr  
           115                  120                  125  
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe  
           130                  135                  140

&lt;210&gt; 1456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g373 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(82)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1456

Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His  
   1                  5                  10                  15  
 Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu  
           20                  25                  30  
 Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys  
           35                  40                  45  
 Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile  
           50                  55                  60  
 Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly  
   65                  70                  75                  80  
 Tyr Ser

&lt;210&gt; 1457

&lt;211&gt; 207

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g374 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(207)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1457

Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe  
   1                  5                  10                  15  
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys  
           20                  25                  30  
 Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

```

      35      40      45
Xaa Trp Ala Leu Met Cys Val Leu Glu Asn Lys Thr Tyr Ala Ser Val
 50      55      60
Arg Leu Val Xaa Arg Phe Gly Trp Xaa Lys Leu Ala Asn Xaa Met Ser
65      70      75      80
Val Leu Tyr Leu Glu Ala Asn Leu Gly Asn Met Asp Asn Ala Leu Leu
      85      90      95
Lys Xaa Leu Lys Arg Asn Tyr Phe Val Phe Val Phe Thr Ser Phe Leu
      100      105      110
Phe Gly Cys Ile Ala Phe Lys Xaa Lys Glu Ile Phe Tyr Pro Tyr Thr
      115      120      125
Ser Ile Cys Ile Tyr His Leu Leu Met Met Glu Arg Lys Val Ser Cys
      130      135      140
Leu Thr Leu Ile Cys Leu Ala Xaa Asp Leu Xaa His Phe Xaa Cys Ser
      145      150      155      160
Leu Val Thr Val Leu Ser Leu Glu Cys Xaa Gln Leu Asp Ile Cys Asn
      165      170      175
Val Val Thr Tyr Phe Asn Thr Met Val Xaa Ser Thr Thr Gly Ser Asn
      180      185      190
Ser Xaa Thr Pro Asn His Ser Val Leu Ile Cys Asn Met Leu Lys
      195      200      205

```

&lt;210&gt; 1458

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g375 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1458

```

Met Arg Asn Leu Ser Gly Gly His Val Glu Glu Phe Val Leu Val Gly
 1      5      10      15
Phe Pro Thr Thr Pro Pro Leu Gln Leu Leu Leu Phe Val Leu Phe Phe
      20      25      30
Ala Ile Tyr Leu Leu Thr Leu Leu Glu Asn Ala Leu Ile Val Phe Thr
      35      40      45
Ile Trp Leu Ala Pro Ser Leu His Arg Pro Met Tyr Phe Phe Leu Gly
      50      55      60
His Leu Ser Phe Leu Glu Leu Trp Tyr Ile Asn Val Thr Ile Pro Arg
      65      70      75      80
Leu Leu Ala Ala Phe Leu Thr Gln Asp Gly Arg Val Ser Tyr Val Gly
      85      90      95
Cys Met Thr Gln Leu Tyr Phe Phe Ile Ala Leu Ala Cys Thr Glu Cys
      100      105      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gly
      115      120      125
Pro Leu Leu Tyr Pro Ser Leu Met Pro Ser Ser Leu Ala Thr Arg Leu
      130      135      140
Ala Ala Ala Ser Trp Gly Ser Gly Phe Phe Ser Ser Met Met Lys Leu
      145      150      155      160
Leu Phe Ile Ser Gln Leu Ser Tyr Cys Gly Pro Asn Ile Ile Asn His
      165      170      175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Asn Leu Thr Cys Ser Asp Lys
      180      185      190
Glu Gln Ala Glu Leu Val Asp Phe Leu Leu Ala Leu Val Met Ile Leu
      195      200      205
Leu Pro Leu Leu Ala Val Val Ser Ser Tyr Thr Ala Ile Ile Ala Ala
      210      215      220
Ile Leu Arg Ile Pro Thr Ser Arg Gly Arg His Lys Ala Phe Ser Thr
      225      230      235      240

```



```
<210> 1459
<211> 322
<212> PRT
<213> Unknown (H38g376 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(322)
<223> Xaa = Any Amino Acid
```

745

290	295	300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro		
305	310	315
Phe Ser		320

<210> 1460  
 <211> 186  
 <212> PRT  
 <213> Unknown (H38g377 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(186)  
 <223> Xaa = Any Amino Acid

<400> 1460  
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu  
 1 5 10 15  
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser  
 20 25 30  
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn  
 35 40 45  
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val  
 50 55 60  
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr  
 65 70 75 80  
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp  
 85 90 95  
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly  
 100 105 110  
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His  
 115 120 125  
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr  
 130 135 140  
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg  
 145 150 155 160  
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr  
 165 170 175  
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu  
 180 185

<210> 1461  
 <211> 336  
 <212> PRT  
 <213> Unknown (H38g378 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(336)  
 <223> Xaa = Any Amino Acid

<400> 1461  
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe  
 20 25 30

Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys  
 115 120 125  
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala  
 145 150 155 160  
 Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val  
 165 170 175  
 Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala  
 180 185 190  
 Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala  
 195 200 205  
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys  
 210 215 220  
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys  
 225 230 235 240  
 Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr  
 245 250 255  
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro  
 260 265 270  
 Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met  
 275 280 285  
 Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val  
 290 295 300  
 Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile  
 305 310 315 320  
 Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys  
 325 330 335

&lt;210&gt; 1462

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g379 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1462

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met  
 1 5 10 15  
 Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe  
 20 25 30  
 Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg  
 35 40 45  
 Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro  
 50 55 60  
 Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu

65					70					75					80
Cys	Thr	Cys	Leu	Asp	Thr	Phe	Thr	Lys	Ser	Tyr	Ile	Thr	Xaa	Ile	Arg
				85					90					95	
Gly	Leu	Lys	Gly	Phe	Asn	His	Leu	Cys	Phe	Leu	Leu	His	Tyr	Cys	His
			100					105					110		
Cys	Ala	Arg	Ala	Gln	Val	Ser	Xaa	Asn	Ala	Pro	Trp	Ser	Leu	Ala	Gln
		115					120					125			
Arg	Cys	Gln	Pro	Asn	Met	Leu	Ile	Arg	Xaa	Leu	Phe	Cys	Leu	Lys	Leu
	130					135					140				
Val	Val	His	Asp	Arg	Leu	Xaa	His	Val	Leu	Ser	Leu	Leu			
145					150					155					

&lt;210&gt; 1463

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g380 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1463

Met	Lys	Ile	Asn	Gln	Thr	Ile	Leu	Lys	Glu	Phe	Ile	Leu	Val	Gly	Phe
1				5					10					15	
Ser	Val	Tyr	Pro	His	Val	Gln	Thr	Phe	Leu	Phe	Val	Val	Phe	Phe	Cys
			20					25					30		
Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Leu	Thr	Ile	Met	Gly	Leu	Thr
		35					40					45			
Xaa	Val	Asp	Arg	Ser	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Ala
	50					55				60					
Leu	Ser	Phe	Ser	Glu	Thr	Cys	Tyr	Thr	Leu	Thr	Ile	Val	Pro	Lys	Met
65					70				75					80	
Leu	Glu	Asp	Leu	Leu	Ala	Lys	Asp	Arg	Ser	Ile	Ser	Val	Thr	Gly	Cys
			85						90					95	
Ser	Leu	Gln	Met	Cys	Phe	Phe	Leu	Gly	Leu	Gly	Gly	Thr	Asn	Cys	Ile
		100						105					110		
Ile	Leu	Thr	Leu	Met	Gly	Tyr	Asp	Arg	Phe	Leu	Ala	Ile	Cys	Asn	Pro
		115					120					125			
Leu	Arg	Tyr	Pro	Leu	Leu	Met	Thr	Asn	Ile	Val	Cys	Gly	Gln	Leu	Val
	130					135					140				
Ala	Ser	Ala	Cys	Thr	Ala	Gly	Phe	Phe	Ile	Ser	Leu	Thr	Glu	Thr	Ala
145					150					155					160
Leu	Ile	Phe	Arg	Asp	Ser	Phe	Cys	Arg	Pro	Asn	Leu	Val	Lys	His	Phe
			165						170					175	
Phe	Cys	His	Met	Leu	Ala	Val	Ile	Arg	Leu	Ser	Cys	Ile	Asp	Ser	Asn
		180						185					190		
His	Thr	Glu	Phe	Ile	Ile	Thr	Leu	Ile	Ser	Val	Ser	Gly	Leu	Leu	Gly
	195						200					205			
Thr	Leu	Leu	Leu	Ile	Ile	Leu	Thr	Asp	Val	Phe	Ile	Ile	Ser	Thr	Val
	210					215					220				
Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Thr	Thr	Cys
225					230					235					240
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Phe	Gly	Phe	Ala	Ser	Ile
			245						250					255	
Val	Tyr	Leu	Lys	Pro	Glu	Ala	Ser	Gly	Asp	Asp	Thr	Leu	Ile	Ala	Val
		260						265					270		
Pro	Tyr	Thr	Val	Ile	Thr	Pro	Phe	Leu	Ser	Pro	Ile	Ile	Phe	Ser	Leu
		275					280						285		

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr  
 290 295 300  
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu  
 305 310 315 320  
 Gly Leu Asn Val Pro  
 325

<210> 1464  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g381 protein)

<220>  
 <223> Synthetic construct

<400> 1464  
 Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu  
 20 25 30  
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg  
 65 70 75 80  
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala  
 115 120 125  
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu  
 130 135 140  
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr  
 145 150 155 160  
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His  
 165 170 175  
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu  
 195 200 205  
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
 245 250 255  
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln  
 260 265 270  
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile  
 275 280 285  
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala  
 290 295 300  
 Phe Arg Gly Arg Leu Leu Gly Lys Gly  
 305 310

<210> 1465  
 <211> 289  
 <212> PRT  
 <213> Unknown (H38g382 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1465

```

Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65           70           75           80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85           90           95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

&lt;210&gt; 1466

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g383 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Ile Ile Thr Val  
 35 40 45  
 Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser  
 50 55 60  
 Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Ser Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys  
 85 90 95  
 Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys  
 100 105 110  
 Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro  
 115 120 125  
 Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr  
 130 135 140  
 Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala  
 145 150 155 160  
 Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile  
 165 170 175  
 Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg  
 180 185 190  
 Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile  
 195 200 205  
 Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala  
 210 215 220  
 Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser  
 225 230 235 240  
 Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val  
 245 250 255  
 Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp  
 260 265 270  
 Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys  
 290 295 300  
 His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly  
 305 310 315

&lt;210&gt; 1467

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g384 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1467

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile  
 1 5 10 15  
 Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu  
 20 25 30  
 Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr  
 35 40 45  
 Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 50 55 60  
 Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu  
 65 70 75 80  
 Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr  
 85 90 95  
 Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 100 105 110  
 Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

115 120 125

Val

<210> 1468  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g385 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(162)  
 <223> Xaa = Any Amino Acid

<400> 1468  
 Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu  
 1 5 10 15  
 Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr  
 20 25 30  
 Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val  
 35 40 45  
 Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met  
 50 55 60  
 Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met  
 65 70 75 80  
 Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg  
 85 90 95  
 Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr  
 100 105 110  
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu  
 115 120 125  
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser  
 130 135 140  
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr  
 145 150 155 160  
 Val Gln

<210> 1469  
 <211> 327  
 <212> PRT  
 <213> Unknown (H38g386 protein)

<220>  
 <223> Synthetic construct

<400> 1469  
 Met Leu Thr Pro Asn Asn Ala Cys Ser Val Pro Thr Ser Phe Arg Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Ile Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Leu Gly Asn Ile Thr Ile Leu  
 35 40 45  
 Ala Val Val Arg Met Glu Tyr Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Val Ile Asp Leu Val Leu Ser Thr Ser Thr Met  
 65 70 75 80  
 Pro Lys Leu Leu Ala Ile Phe Trp Phe Gly Ala His Asn Ile Gly Val  
 85 90 95



```

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val
      100                      105                      110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile
      115                      120                      125
Cys Asp Pro Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly
      130                      135                      140
Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro
      145                      150                      155                      160
Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile
      165                      170                      175
Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys
      180                      185                      190
Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe
      195                      200                      205
Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met
      210                      215                      220
Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys
      225                      230                      235                      240
Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr
      245                      250                      255
Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val
      260                      265                      270
Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile
      275                      280                      285
Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile
      290                      295                      300
Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile
      305                      310                      315                      320
Lys Ala Arg Thr Gln Thr Arg
      325

```

&lt;210&gt; 1470

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g387 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1470

```

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
  1          5          10          15
Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
  20          25          30
Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
  35          40          45
Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
  50          55          60
Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
  65          70          75          80
Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
  85          90          95
His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
  100         105         110
Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
  115         120         125
Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

```

```

      130              135              140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val
145              150              155              160
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile
      165              170              175
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr
      180              185              190
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn
      195              200              205
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala
      210              215              220
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ala Ile Leu Arg Ile
225              230              235              240
Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His
      245              250              255
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile
      260              265              270
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met
      275              280              285
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met
      290              295              300
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser
305              310              315              320
His Ser Ser

```

&lt;210&gt; 1471

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g388 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1471

```

Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile
1      5      10      15
Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val
      20      25      30
Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser
      35      40      45
Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe
      50      55      60
Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr
      65      70      75      80
Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu
      85      90      95
Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu
      100      105      110
Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser
      115      120      125
Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Gly Pro Cys
      130      135      140
Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe
145      150      155      160
Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile
      165      170      175

```

Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg  
 180 185 190  
 Lys Trp Asp Ala His Ser Ser Val Lys Phe  
 195 200

<210> 1472  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g389 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(311)  
 <223> Xaa = Any Amino Acid

<400> 1472  
 Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
 65 70 75 80  
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
 85 90 95  
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
 100 105 110  
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
 130 135 140  
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
 145 150 155 160  
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
 180 185 190  
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu  
 195 200 205  
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser  
 210 215 220  
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr  
 225 230 235 240  
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile  
 245 250 255  
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His  
 260 265 270  
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro  
 275 280 285  
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu  
 290 295 300  
 Ser Tyr Ile Gln Arg Ala Arg  
 305 310

<210> 1473  
 <211> 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g390 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20           25           30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
305          310          315

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&lt;210&gt; 1474

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g391 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1474

```

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
          20           25           30
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
145          150          155          160
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
          165          170          175
His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
          180          185          190
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
          210          215          220
Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser
305          310          315          320
Gly Ala Cys Cys Ala Pro
          325

```

&lt;210&gt; 1475

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g392 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1475

```

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1           5           10           15
Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
          20           25           30
Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
          35           40           45
Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100          105          110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115          120          125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130          135          140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
      145          150          155          160
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180          185          190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195          200          205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
      210          215          220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
      225          230          235          240
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245          250          255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260          265          270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
      290          295          300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
      305          310

```

&lt;210&gt; 1476

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g393 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1      5      10      15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
20      25      30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
35      40      45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
50      55      60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
65      70      75      80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
85      90      95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
100      105      110
Pro Arg Lys Asp Val
115

```

&lt;210&gt; 1477

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g394 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
      20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
      35           40           45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
      50           55           60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65           70           75           80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
      85           90           95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
      100          105          110
Ser Phe Leu Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
      130          135          140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145          150          155          160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
      165          170          175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
      180          185          190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
      195          200          205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
      210          215          220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225          230          235          240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
      245          250          255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
      260          265          270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
      275          280          285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
      290          295          300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
305          310          315

```

&lt;210&gt; 1478

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g395 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
 1           5           10           15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
      20           25           30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```

      35      40      45
Ile Ile Tyr Leu Leu Thr Val Leu Gly Asn Gln Leu Ile Ile Ile Leu
  50      55      60
Ile Phe Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
  65      70      75      80
Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Thr Ser Ile Val Pro Gln
      85      90      95
Val Leu Val His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Tyr Gly
      100      105      110
Cys Met Thr Gln Ile Ile Val Phe Leu Leu Val Gly Cys Thr Glu Cys
      115      120      125
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys
      130      135      140
Pro Leu Tyr Tyr Ser Thr Ile Met Thr Gln Arg Val Cys Leu Trp Leu
      145      150      155      160
Ser Phe Arg Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr
      165      170      175
Ser Phe Thr Phe His Leu Pro Tyr Trp Gly Gln Asn Ile Ile Asn His
      180      185      190
Tyr Phe Cys Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ile Asp Thr
      195      200      205
Tyr Ser Thr Glu Met Ala Ile Phe Ser Met Gly Val Val Ile Leu Leu
      210      215      220
Ala Pro Val Ser Leu Ile Leu Gly Ser Tyr Trp Asn Ile Ile Ser Thr
      225      230      235      240
Val Ile Gln Met Gln Ser Gly Glu Gly Arg Leu Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Gly Ile
      260      265      270
Phe Thr Tyr Met Arg Pro Asn Ser Lys Thr Thr Lys Glu Leu Asp Lys
      275      280      285
Met Ile Ser Val Phe Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Ile
      290      295      300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Arg Lys Leu
      305      310      315      320
Val Gly Arg Lys Cys Phe Ser His Arg Gln
      325      330

```

&lt;210&gt; 1479

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g396 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(227)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1479

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
  1      5      10      15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
      20      25      30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
      35      40      45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
      50      55      60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
      65      70      75      80

```



Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe  
                             85                            90                            95  
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser  
                             100                            105                            110  
 Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly  
                             115                            120                            125  
 Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys  
                             130                            135                            140  
 Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser  
 145                            150                            155                            160  
 Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala  
                             165                            170                            175  
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile  
                             180                            185                            190  
 Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr  
                             195                            200                            205  
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser  
                             210                            215                            220  
 Lys Val Lys  
 225

&lt;210&gt; 1480

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g397 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1480

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe  
 1                            5                            10                            15  
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val  
                             20                            25                            30  
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser  
                             35                            40                            45  
 Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr  
                             50                            55                            60  
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser  
 65                            70                            75                            80  
 Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile  
                             85                            90                            95  
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
                             100                            105                            110  
 Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu  
                             115                            120                            125  
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu  
                             130                            135                            140  
 Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe  
 145                            150                            155                            160  
 Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile  
                             165                            170                            175  
 Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys  
                             180                            185                            190  
 Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu  
                             195                            200                            205  
 Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val  
                             210                            215                            220  
 Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala  
 225                            230                            235                            240  
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

			245					250					255				
Ser	Met	Met	Ile	Thr	Tyr	Val	Ser	Pro	Thr	Ser	Gly	His	Glu	Phe	Gly		
			260					265					270				
Met	Gln	Lys	Thr	Val	Thr	Leu	Phe	Tyr	Ser	Val	Val	Thr	Pro	Leu	Ile		
		275						280				285					
Asn	Pro	Val	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Met	Lys	His	Ala	Met		
	290					295				300							
Arg	Asn	Tyr	Thr	Val	Met	Phe	Tyr	Leu	Ser	Arg	Ile	His	Arg	Ala	Thr		
305					310					315					320		
Arg	Asp	Val	Lys	Asp	Val	Phe	Tyr	Leu	Phe	Asn	Phe						
			325						330								

&lt;210&gt; 1481

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g398 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(269)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1481

Phe	Ser	Ser	Ile	Tyr	Ala	Trp	Tyr	Ile	Ser	Asp	Leu	Tyr	Leu	Asn	Tyr		
1			5					10					15				
Leu	Ser	Asn	His	Leu	Ser	Ile	Phe	Lys	Leu	Val	Asp	Trp	Ile	Ile	Asn		
		20						25				30					
Cys	Tyr	Leu	Tyr	Tyr	Phe	Tyr	Ser	Leu	Leu	Thr	Leu	Phe	Xaa	Gln	Phe		
		35					40				45						
Ile	Tyr	Thr	Cys	Glu	Met	Asn	Gln	Phe	Lys	Xaa	Xaa	Gln	Asn	Arg	Asn		
	50					55				60							
Asn	Leu	Thr	Thr	Phe	Xaa	Gly	Tyr	Phe	Tyr	Ser	Gly	Ile	Cys	Gly	Arg		
65				70				75						80			
Arg	Asn	Cys	Thr	Met	Xaa	Leu	Ile	Thr	Ile	Phe	Ile	Leu	Lys	Tyr	Cys		
			85					90					95				
Xaa	His	Gly	Phe	Ile	Thr	Ile	His	Ser	Val	Met	Asp	Ser	Gly	Gln	His		
		100					105					110					
Leu	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Leu	Ile	Leu	Met	Thr	Asp	Glu		
		115				120					125						
Asn	Arg	Asp	Arg	Met	Phe	Met	Gly	Pro	Leu	Thr	Ala	Phe	Pro	Tyr	Thr		
	130				135					140							
Asp	Ala	Thr	Ser	Gln	Asn	Met	His	Tyr	Val	Asn	Phe	Leu	Ile	Ile	Ile		
145				150					155					160			
Leu	Ser	Ile	Leu	Tyr	Ile	Pro	Gly	Pro	Tyr	Thr	Leu	Ile	Leu	Arg	Ala		
		165					170					175					
Met	Leu	Gln	Leu	Leu	Ser	Ala	Ala	Ser	His	Gln	Asn	Ala	Phe	Ser	Ile		
		180					185					190					
Arg	Gly	Ser	His	Leu	Ile	Val	Val	Ser	Leu	Phe	Cys	Glu	Thr	Ile	Met		
		195				200					205						
Met	Met	Cys	Val	Asn	Leu	Ile	Ser	Asp	His	Leu	Val	Xaa	Met	Lys	Met		
	210				215					220							
Thr	Asn	His	Asn	Ile	Ile	Met	Ile	Ser	Ser	Ile	Lys	Thr	Leu	Val	Leu		
225				230					235					240			
Asn	Phe	Val	Asn	Tyr	Thr	Leu	Leu	Asn	Met	Asn	Leu	Lys	Leu	Tyr	Leu		
			245					250						255			
Gln	Phe	Phe	Phe	Tyr	Gly	Met	Ser	Ile	Ser	Gln	Ser	Ser					
		260					265										

&lt;210&gt; 1482

<211> 311  
 <212> PRT  
 <213> Unknown (H38g399 protein)

<220>  
 <223> Synthetic construct

<400> 1482  
 Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe  
 1 5 10 15  
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe  
 20 25 30  
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser  
 35 40 45  
 Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr  
 50 55 60  
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser  
 65 70 75 80  
 Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile  
 85 90 95  
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
 100 105 110  
 Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu  
 115 120 125  
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu  
 130 135 140  
 Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe  
 145 150 155 160  
 Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg  
 165 170 175  
 Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr  
 180 185 190  
 Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro  
 195 200 205  
 Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu  
 210 215 220  
 Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala  
 260 265 270  
 Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu  
 275 280 285  
 Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala  
 290 295 300  
 Leu Lys Lys Phe Trp Gly Thr  
 305 310

<210> 1483  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g400 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(326)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1483

```

Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
 1          5          10          15
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
          20          25          30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
          35          40          45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
          50          55          60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
65          70          75          80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
          85          90          95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
          100          105          110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
          115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
          130          135          140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
145          150          155          160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
          165          170          175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
          180          185          190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
          195          200          205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
          210          215          220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
225          230          235          240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
          245          250          255
Phe Gly Ala Leu Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
          260          265          270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
          275          280          285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
          290          295          300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
305          310          315          320
Glu Thr Lys Gln Thr Ile
          325

```

&lt;210&gt; 1484

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g401 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1          5          10          15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
          20          25          30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
          35          40          45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
          50          55          60

```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly  
 85 90 95  
 Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly  
 100 105 110  
 Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu  
 130 135 140  
 Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile  
 145 150 155 160  
 Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln  
 165 170 175  
 Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile  
 195 200 205  
 Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile  
 210 215 220  
 Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu  
 245 250 255  
 Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala  
 260 265 270  
 Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe  
 290 295 300  
 Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly  
 305 310 315

&lt;210&gt; 1485

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g402 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1485

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg  
 1 5 10 15  
 Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu  
 20 25 30  
 Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg  
 35 40 45  
 Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu  
 50 55 60  
 Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile  
 65 70 75 80  
 Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe  
 85 90 95  
 Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val  
 100 105 110  
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro  
 115 120 125  
 Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp  
 130 135 140  
 Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

145                      150                      155                      160  
 Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro  
                                  165                      170                      175  
 Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu  
                                  180                      185                      190  
 Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser  
                                  195                      200                      205  
 Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro  
                                  210                      215                      220  
 Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu  
 225                                   230                      235                      240  
 Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser  
                                  245                      250                      255  
 Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val  
                                  260                      265                      270  
 Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg  
                                  275                      280                      285  
 Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val  
                                  290                      295                      300  
 Ser Gln Asn  
 305

&lt;210&gt; 1486

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g403 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1486

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr  
 1                      5                      10                      15  
 Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg  
                                  20                      25                      30  
 Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser  
                                  35                      40                      45  
 Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg  
                                  50                      55                      60  
 Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro  
 65                                   70                      75                      80  
 Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu  
                                  85                      90                      95  
 Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly  
                                  100                      105                      110  
 Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg  
                                  115                      120                      125  
 Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His  
                                  130                      135                      140  
 Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile  
 145                                   150                      155                      160  
 Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln  
                                  165                      170                      175  
 Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe  
                                  180                      185                      190  
 Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro  
                                  195                      200                      205  
 Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro  
                                  210                      215                      220  
 Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile  
 225                                   230                      235                      240

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val  
 245 250 255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

Ser Leu Gly Ser Met Asn Asn Ser Gln Ile Ser Thr Val Thr Gln Phe  
 1 5 10 15  
 Val Leu Leu Gly Phe Pro Gly Pro Trp Lys Ile Gln Ile Ile Phe Phe  
 20 25 30  
 Ser Met Ile Leu Leu Val Tyr Ile Phe Thr Leu Thr Gly Asn Met Ala  
 35 40 45  
 Ile Ile Cys Ala Val Arg Trp Asp His Arg Leu His Thr Pro Met Tyr  
 50 55 60  
 Val Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Cys  
 65 70 75 80  
 Thr Val Pro Asn Met Leu Val Asn Phe Phe Ser Lys Thr Lys Thr Ile  
 85 90 95  
 Ser Phe Ser Gly Cys Phe Thr Gln Phe His Phe Phe Ser Ser Leu Gly  
 100 105 110  
 Thr Thr Glu Cys Phe Phe Leu Cys Val Met Ala Tyr Asp Arg Tyr Leu  
 115 120 125  
 Ala Ile Cys His Pro Leu His Tyr Pro Ser Ile Met Thr Gly Gln Leu  
 130 135 140  
 Cys Gly Ile Leu Val Ser Leu Cys Trp Leu Ile Gly Phe Leu Gly His  
 145 150 155 160  
 Ser Ile Ser Ile Phe Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn  
 165 170 175  
 Ile Ile Asp His Phe Leu Cys Asp Val Asp Pro Leu Met Ala Leu Ser  
 180 185 190  
 Ser Ala Pro Thr His Ile Ile Gly His Val Phe His Ser Val Ser Ser  
 195 200 205  
 Leu Phe Ile Asn Leu Thr Met Val Tyr Ile Leu Gly Ser Tyr Thr Leu  
 210 215 220  
 Val Leu Arg Thr Val Leu Xaa Val Pro Ser Ser Ala Gly Trp Gln Lys  
 225 230 235 240  
 Ala Ile Ser Thr Cys Gly Ser His Leu Val Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Ala Ile Met Leu Met Tyr Val Ser Pro Thr Pro Gly Asn Ser Val  
 260 265 270  
 Ala Met His Lys Leu Ile Thr Leu Ile Tyr Ser Val Val Thr Pro Val  
 275 280 285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Tyr Ala  
 290 295 300  
 Leu His His Val Phe Cys Gly Met Arg Ile Ile Gln Arg Ser Xaa Ile  
 305 310 315 320

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1488

```

Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
 1           5           10           15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Leu Phe Phe Ile Pro Met Leu
           20           25           30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
           35           40           45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
           50           55           60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
           85           90           95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
           100          105          110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
           115          120          125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
           130          135          140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
145          150          155          160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
           165          170          175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
           180          185          190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
           195          200          205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
210          215          220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
225          230          235          240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
           245          250          255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
           260          265          270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
           275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
290          295          300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
305          310          315

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&lt;210&gt; 1489

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g406 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1489

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Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
 1           5           10           15

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Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe  
                   20                                  25                                  30  
 Ile Pro Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile  
                   35                                  40                                  45  
 Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr  
                   50                                  55                                  60  
 Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr  
 65                                  70                                  75                                  80  
 Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile  
                   85                                  90                                  95  
 Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly  
                   100                                  105                                  110  
 Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile  
                   115                                  120                                  125  
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu  
                   130                                  135                                  140  
 Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val  
 145                                  150                                  155                                  160  
 Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn  
                   165                                  170                                  175  
 Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala  
                   180                                  185                                  190  
 Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala  
                   195                                  200                                  205  
 Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile  
                   210                                  215                                  220  
 Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala  
 225                                  230                                  235                                  240  
 Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly  
                   245                                  250                                  255  
 Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe  
                   260                                  265                                  270  
 Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe  
                   275                                  280                                  285  
 Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile  
                   290                                  295                                  300  
 Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala  
 305                                  310                                  315

&lt;210&gt; 1490

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g407 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1490

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp  
 1                                  5                                  10                                  15  
 Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu  
                   20                                  25                                  30  
 Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp  
                   35                                  40                                  45  
 Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln  
                   50                                  55                                  60  
 Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala  
 65                                  70                                  75                                  80  
 Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr  
                   85                                  90                                  95  
 Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

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      100      105      110
Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val Leu
      115      120      125
His Ile Pro Tyr Cys Gln Ser Arg Ala Ile Asn His Phe Phe Cys Asp
      130      135      140
Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp Val Tyr Glu
145      150      155      160
Gly Thr Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile
      165      170      175
Ala Ile Ser Cys Ser Tyr Gly Arg Val Leu Leu Ala Val Tyr His Met
      180      185      190
Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys Ser Thr His
      195      200      205
Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu
      210      215      220
Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val
225      230      235      240
Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
      245      250      255
Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg Ile
      260      265      270
Cys Ser Val Lys Met
      275

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&lt;210&gt; 1491

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g408 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(241)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1491

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1      5      10      15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20      25      30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35      40      45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50      55      60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
65      70      75      80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85      90      95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100      105      110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115      120      125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130      135      140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
145      150      155      160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165      170      175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180      185      190

```

Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu  
 195 200 205  
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser  
 210 215 220  
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val  
 225 230 235 240  
 Gly

&lt;210&gt; 1492

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g409 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu  
 20 25 30  
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val  
 35 40 45  
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile  
 130 135 140  
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile  
 145 150 155 160  
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His  
 165 170 175  
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu  
 195 200 205  
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr  
 210 215 220  
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu  
 245 250 255  
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln  
 260 265 270  
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln  
 290 295 300  
 Leu Lys Arg Ile Gly Ile Leu Ala  
 305 310

&lt;210&gt; 1493

&lt;211&gt; 212

<212> PRT  
 <213> Unknown (H38g410 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(212)  
 <223> Xaa = Any Amino Acid

<400> 1493  
 Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu  
 1 5 10 15  
 Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu  
 20 25 30  
 Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile  
 35 40 45  
 Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu  
 50 55 60  
 Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val  
 65 70 75 80  
 Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe  
 85 90 95  
 Thr Gly Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala  
 100 105 110  
 Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val  
 130 135 140  
 Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala  
 145 150 155 160  
 His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile  
 165 170 175  
 Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met  
 180 185 190  
 Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro  
 195 200 205  
 Trp Ala Gly Pro  
 210

<210> 1494  
 <211> 263  
 <212> PRT  
 <213> Unknown (H38g411 protein)

<220>  
 <223> Synthetic construct

<400> 1494  
 Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe  
 1 5 10 15  
 Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu  
 20 25 30  
 Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val  
 35 40 45  
 Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His  
 50 55 60  
 Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met  
 65 70 75 80  
 Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala  
 85 90 95

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu  
 100 105 110  
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val  
 130 135 140  
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val  
 145 150 155 160  
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His  
 165 170 175  
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr  
 180 185 190  
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile  
 195 200 205  
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr  
 210 215 220  
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu  
 245 250 255  
 Phe Leu Tyr Val Lys Pro Lys  
 260

&lt;210&gt; 1495

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g412 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu  
 20 25 30  
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val  
 35 40 45  
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly  
 85 90 95  
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met  
 130 135 140  
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val  
 145 150 155 160  
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His  
 165 170 175  
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr  
 180 185 190  
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu  
 195 200 205  
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala  
 210 215 220  
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225		230		235		240									
Cys	Ala	Ser	His	Leu	Ala	Val	Val	Leu	Ile	Phe	Phe	Gly	Ser	Ile	Ile
		245		250		255									
Phe	Met	Tyr	Val	Arg	Leu	Lys	Lys	Ser	Tyr	Ser	Leu	Thr	Leu	Asp	Arg
		260		265		270									
Thr	Leu	Ala	Ile	Val	Tyr	Ser	Val	Leu	Thr	Pro	Met	Val	Asn	Pro	Ile
		275		280		285									
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Ile	Ile	Lys	Ala	Ile	Lys	Arg	Thr
		290		295		300									
Ile	Phe	Gln	Lys	Gly	Asp	Lys	Ala	Ser	Leu	Ala	His	Leu			
305				310						315					

&lt;210&gt; 1496

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g413 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1496

Met	Gln	Gly	Leu	Asn	His	Thr	Ser	Val	Ser	Glu	Phe	Ile	Leu	Val	Gly
1			5					10					15		
Phe	Ser	Ala	Phe	Pro	His	Leu	Gln	Leu	Met	Leu	Phe	Leu	Leu	Phe	Leu
		20					25					30			
Leu	Met	Tyr	Leu	Phe	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Met	Ala	Thr
		35				40						45			
Val	Trp	Ser	Glu	Arg	Ser	Leu	His	Met	Pro	Met	Tyr	Leu	Phe	Leu	Cys
	50				55					60					
Ala	Leu	Ser	Ile	Thr	Glu	Ile	Leu	Tyr	Thr	Val	Ala	Ile	Ile	Pro	Arg
65				70					75					80	
Met	Leu	Ala	Asp	Leu	Leu	Ser	Thr	Gln	Arg	Ser	Ile	Ala	Phe	Leu	Ala
			85					90						95	
Cys	Ala	Ser	Gln	Met	Phe	Phe	Ser	Phe	Ser	Phe	Gly	Phe	Thr	His	Ser
		100					105						110		
Phe	Leu	Leu	Thr	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
		115				120						125			
Pro	Leu	Arg	Tyr	Asn	Val	Leu	Met	Ser	Leu	Arg	Gly	Cys	Thr	Cys	Arg
	130				135						140				
Val	Gly	Cys	Ser	Trp	Ala	Gly	Gly	Leu	Val	Met	Gly	Met	Val	Val	Thr
145				150					155					160	
Ser	Ala	Ile	Phe	His	Leu	Ala	Phe	Cys	Gly	His	Lys	Glu	Ile	His	His
			165					170						175	
Phe	Phe	Cys	His	Val	Pro	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Gly	Asp	Asp
		180					185						190		
Val	Leu	Val	Val	Ala	Lys	Gly	Val	Gly	Leu	Val	Cys	Ile	Thr	Ala	Leu
		195				200					205				
Leu	Gly	Cys	Phe	Leu	Leu	Ile	Leu	Leu	Ser	Tyr	Ala	Phe	Ile	Val	Ala
	210				215					220					
Ala	Ile	Leu	Lys	Ile	Pro	Ser	Ala	Glu	Gly	Arg	Asn	Lys	Ala	Phe	Ser
225				230					235					240	
Thr	Cys	Ala	Ser	His	Leu	Thr	Val	Val	Val	Val	His	Tyr	Gly	Phe	Ala
			245					250						255	
Ser	Val	Ile	Tyr	Leu	Lys	Pro	Lys	Gly	Pro	Gln	Ser	Pro	Glu	Gly	Asp
		260						265					270		
Thr	Leu	Met	Gly	Ile	Thr	Tyr	Thr	Val	Leu	Thr	Pro	Phe	Leu	Ser	Pro
	275					280						285			
Ile	Ile	Phe	Ser	Leu	Arg	Asn	Lys	Glu	Leu	Lys	Val	Ala	Met	Lys	Lys
	290				295						300				
Thr	Cys	Phe	Thr	Lys	Leu	Phe	Pro	Gln	Asn	Cys					
305				310						315					

<210> 1497  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g414 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid

<400> 1497  
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
 20 25 30  
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His  
 165 170 175  
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315

<210> 1498  
 <211> 157  
 <212> PRT  
 <213> Unknown (H38g415 protein)

<220>

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1498

```

Val Ser Pro Leu Trp Glu Cys Val Ser Xaa Gln Arg Ser Pro His Phe
 1          5          10          15
Leu Cys Ser Gly Asp Ser Val Phe Cys Leu Val His Ser Val Gly Cys
          20          25          30
Cys Thr Leu Leu Leu Ser Gln Ser Leu Arg Leu Leu Ser Val Phe Leu
          35          40          45
Leu Ser Ser Cys Ala Ala Ser Trp Lys Lys Val His Ser Met Asn Leu
          50          55          60
Tyr Thr Pro Phe Cys Leu Ser Lys Trp Xaa Asn His Val Asn Asn Ala
65          70          75          80
Phe Asn Leu Pro Ser Trp Lys Lys Ser Lys Ser Val Val Thr Met Phe
          85          90          95
Xaa Gly Pro Ala Met Ile Thr Tyr Leu Arg Ser Asp Ser Xaa Tyr Asn
          100          105          110
Pro Thr Val Gly Lys Gln Leu Val Leu Phe Tyr Ser Ile Val Ser Ala
          115          120          125
Phe Ile Lys Pro Ile Ile Ser Ser Leu Arg Asn Lys Asp Val Lys Gly
          130          135          140
Ala Ser Trp Lys Val Leu Arg Val Lys Gly Thr Ala Gln
145          150          155

```

&lt;210&gt; 1499

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g416 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1499

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1          5          10          15
Phe Pro Pro Ser Arg Ile Asp Leu Phe Phe Phe Ile Leu Phe Val Leu
          20          25          30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
          35          40          45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50          55          60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Ala Ser Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Ile Gly Cys
          85          90          95
Gly Ile Gln Ser Phe Phe Phe Met Thr Phe Ala Gly Ala Glu Ala Leu
          100          105          110
Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro
          115          120          125
Leu His Tyr Pro Ile Arg Met Ser Lys Arg Met Tyr Val Leu Met Ile
          130          135          140
Thr Gly Ser Trp Met Ile Gly Ser Ile Asn Ser Cys Ala His Thr Val
145          150          155          160
Tyr Ala Phe Arg Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe
          165          170          175
Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys Thr Asp Thr Trp
          180          185          190

```



Val Tyr Glu Tyr Thr Val Phe Leu Ser Ser Thr Ile Phe Leu Val Phe  
 195 200 205  
 Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Trp Val Leu Leu Ala Val  
 210 215 220  
 Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys  
 225 230 235 240  
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Leu Arg Tyr  
 245 250 255  
 Thr Tyr Leu Cys Pro Arg Ser Leu Phe Ile Ser Thr Glu Asp Lys Val  
 260 265 270  
 Gly Gly Gly Gly Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile  
 275 280 285

&lt;210&gt; 1500

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g417 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1500

Met Asp Lys Glu Asn Ser Ser Met Val Thr Glu Phe Ile Phe Met Gly  
 1 5 10 15  
 Ile Thr Gln Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu  
 20 25 30  
 Ile Val Tyr Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu  
 35 40 45  
 Ile Thr Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg  
 65 70 75 80  
 Met Leu Ala Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser  
 85 90 95  
 Cys Ala Thr Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys  
 100 105 110  
 Tyr Val Leu Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu  
 130 135 140  
 Met Leu Gly Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr  
 145 150 155 160  
 Thr Leu Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Phe Cys Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Tyr Ile Ser Glu Ile Leu Leu Phe Ser Leu Cys Gly Phe Ile Glu Phe  
 195 200 205  
 Ser Thr Ile Leu Ile Ile Phe Ile Ser Tyr Thr Phe Ile Leu Val Ala  
 210 215 220  
 Ile Ile Arg Met Arg Ser Ala Glu Gly Arg Leu Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Gly Ile Thr Leu Phe Tyr Gly Thr Val Met  
 245 250 255  
 Phe Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Leu Asp Gln Asp Lys  
 260 265 270  
 Trp Ala Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Lys Lys Leu  
 290 295 300  
 Ile Gly Lys Lys Ser Gln

305

310

&lt;210&gt; 1501

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g418 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1501

Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Arg	Gln	Leu	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55				60					
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70				75					80	
Lys	Met	Ile	Val	Asp	Ile	Arg	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
			85					90					95		
Gly	Cys	Leu	Thr	Gln	Thr	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
		100						105				110			
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Gln	Phe	Val	Ala	Ile
	115					120					125				
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Val	Met	Asn	Pro	Cys	Phe	Cys	Gly
	130					135				140					
Phe	Leu	Val	Leu	Leu	Thr	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln
145					150				155					160	
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	Glu
			165					170					175		
Ile	Pro	Asn	Phe	Trp	Asp	Pro	Ser	Pro	Leu	Pro	His	Leu	Ala	Cys	
	180					185					190				
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
	195					200					205				
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	Ile
	210				215						220				
Val	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala
225					230					235				240	
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly
			245					250					255		
Thr	Gly	Ile	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg
		260				265							270		
Lys	Ala	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu
	275					280						285			
Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Lys	Ser	Val	Leu
	290					295					300				
Arg	Trp	Leu	His	Gly	Ser	Ser	Val	Xaa	Ser	Gln	His	Leu	Leu	Ile	Cys
305					310					315				320	
Cys	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser	Arg	Val	Lys	
			325					330						335	

&lt;210&gt; 1502

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g419 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1           5           10           15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
      20           25           30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
      35           40           45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
      50           55           60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
      65           70           75           80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
      85           90           95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
      100          105          110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
      115          120          125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
      130          135          140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
      145          150          155          160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
      165          170          175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
      180          185          190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
      195          200          205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
      210          215          220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
      225          230          235          240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
      245          250          255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
      260          265          270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
      290          295          300

```

&lt;210&gt; 1503

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g420 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1503

```

Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1           5           10           15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```

```
<210> 1504
<211> 315
<212> PRT
<213> Unknown (H38g421 protein)
```

<220>  
<223> Synthetic construct

<400> :1504																
Met	Ser	Ile	Thr	Lys	Ala	Trp	Asn	Ser	Ser	Ser	Val	Thr	Met	Phe	Ile	
1				5					10					15		
Leu	Leu	Gly	Phe	Thr	Asp	His	Pro	Glu	Leu	Gln	Ala	Leu	Leu	Phe	Val	
			20					25					30			
Thr	Phe	Leu	Gly	Ile	Tyr	Leu	Thr	Thr	Leu	Ala	Trp	Asn	Leu	Ala	Leu	
		35					40					45				
Ile	Phe	Leu	Ile	Arg	Gly	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	
	50					55					60					
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Ile	Cys	Tyr	Ser	Ser	Ala	Val	
65					70					75					80	
Ala	Pro	Asn	Met	Leu	Thr	Asp	Phe	Phe	Trp	Glu	Gln	Lys	Thr	Ile	Ser	
				85					90					95		

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu  
 100 105 110  
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala  
 115 120 125  
 Ile Ser Ser Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys  
 130 135 140  
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu  
 145 150 155 160  
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile  
 165 170 175  
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys  
 180 185 190  
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr  
 195 200 205  
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile  
 210 215 220  
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala  
 225 230 235 240  
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly  
 245 250 255  
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly  
 260 265 270  
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu  
 275 280 285  
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu  
 290 295 300  
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser  
 305 310 315

&lt;210&gt; 1505

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g422 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu  
 1 5 10 15  
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu  
 20 25 30  
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile  
 35 40 45  
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr  
 65 70 75 80  
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile  
 85 90 95  
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly  
 100 105 110  
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys  
 130 135 140  
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

145		150		155		160
Val Ile Asn Val	Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro Asn Ile					
	165		170		175	
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys						
	180		185		190	
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile						
	195		200		205	
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile						
	210		215		220	
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala						
225	230		235		240	
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly						
	245		250		255	
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala						
	260		265		270	
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu						
	275		280		285	
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg						
	290		295		300	
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu						
305	310		315			

&lt;210&gt; 1506

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g423 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(340)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1506

Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly														
1		5		10		15								
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe														
	20		25		30									
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr														
	35		40		45									
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu														
	50		55		60									
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro														
65	70		75		80									
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln														
	85		90		95									
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn														
	100		105		110									
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys														
	115		120		125									
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln														
	130		135		140									
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln														
145	150		155		160									
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser														
	165		170		175									
His Phe Phe Cys Asp Val Arg His Leu Lys Leu Ala Cys Thr Asp														
	180		185		190									
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu														
	195		200		205									

Val Leu Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser  
 210 215 220  
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala  
 245 250 255  
 Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp  
 260 265 270  
 Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val  
 275 280 285  
 Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala  
 290 295 300  
 Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala  
 305 310 315 320  
 Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile  
 325 330 335  
 Met Pro Leu Cys  
 340

&lt;210&gt; 1507

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g424 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1507

Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser  
 1 5 10 15  
 Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp  
 20 25 30  
 Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Thr  
 35 40 45  
 Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly  
 50 55 60  
 Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys  
 65 70 75 80  
 Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu  
 85 90 95  
 Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser  
 100 105 110  
 Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr  
 115 120 125  
 Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala  
 130 135 140  
 Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro  
 145 150 155 160  
 Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln  
 165 170 175  
 Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr  
 180 185 190  
 Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly  
 195 200 205  
 Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser  
 210 215 220  
 Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

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<210> 1508
<211> 315
<212> PRT
<213> Unknown (H38g425 protein)
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<400>	1508																		
Met	Phe	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly				
1				5					10					15					
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu				
			20					25					30						
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu				
		35					40					45							
Ile	Arg	Thr	Asn	Ser	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly				
	50					55					60								
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn				
65					70						75				80				
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly				
			85						90					95					
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe				
			100					105					110						
Tyr	Ile	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser				
		115					120					125							
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Val	Cys	Leu				
	130					135					140								
Val	Thr	Ile	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Ser	Gly	Phe	Ser	Gln	Ser				
145					150						155			160					
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His				
				165					170					175					
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr				
			180					185					190						
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Asn	Leu	Ser				
		195					200					205							
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala				
	210					215					220								
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr				
225					230					235					240				
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe				
				245					250					255					
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys				
			260					265					270						
Ile	Thr	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu				
		275					280					285							
Ile	Tyr	Ser	Leu	Arg	Asn	Thr	Asp	Val	Ile	Leu									



<210> 1509  
 <211> 257  
 <212> PRT  
 <213> Unknown (H38g426 protein)

<220>  
 <223> Synthetic construct

<400> 1509  
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala  
 1 5 10 15  
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg  
 20 25 30  
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala  
 35 40 45  
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg  
 50 55 60  
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys  
 65 70 75 80  
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Lys Ala Val Ala  
 85 90 95  
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln  
 100 105 110  
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu  
 115 120 125  
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu  
 130 135 140  
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr  
 145 150 155 160  
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His  
 165 170 175  
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala  
 180 185 190  
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His  
 195 200 205  
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu  
 210 215 220  
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys  
 225 230 235 240  
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro  
 245 250 255  
 Leu

<210> 1510  
 <211> 358  
 <212> PRT  
 <213> Unknown (H38g427 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(358)  
 <223> Xaa = Any Amino Acid

<400> 1510  
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro  
 1 5 10 15  
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

```
<210> 1511
<211> 313
<212> PRT
<213> Unknown (H38g428 protein)
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<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid
```

```

<400> 1511
Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu
 1             5             10             15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro
      20             25             30

```

Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Ile  
 35 40 45  
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu  
 50 55 60  
 Ala Gly Thr Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys Ala Leu  
 65 70 75 80  
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile  
 85 90 95  
 Thr Gln Met Phe Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile  
 100 105 110  
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu  
 115 120 125  
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu  
 130 135 140  
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu  
 145 150 155 160  
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr  
 165 170 175  
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val  
 180 185 190  
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp  
 195 200 205  
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe  
 210 215 220  
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly  
 225 230 235 240  
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr  
 245 250 255  
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile  
 260 265 270  
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met  
 290 295 300  
 Leu Ser Val Val Gly Lys Ser Xaa Asp  
 305 310

&lt;210&gt; 1512

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g429 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu  
 1 5 10 15  
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu  
 20 25 30  
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe  
 35 40 45  
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met  
 50 55 60  
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr  
 65 70 75 80  
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr  
 85 90 95  
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu  
 100 105 110  
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

```

      115              120              125
Met Ala Ile Cys Asn Pro Leu His Tyr Ser Ser Lys Met Ser Arg Ala
      130              135              140
Val Cys Ile Cys Leu Val Thr Phe Pro Tyr Phe Trp Gly Ser Met Val
      145              150              155
Gly Thr Met Gln Val Ile Leu Thr Ser Arg Leu Ser Phe Phe Gly Pro
      165              170              175
Asn Thr Ile Asn His Phe Tyr Cys Thr Asp Pro Pro Leu Leu Met Leu
      180              185              190
Thr Ser Ser Asp Thr Tyr Ile Lys Gln Thr Ala Leu Phe Val Ser Ala
      195              200              205
Gly Ile Asn Leu Thr Val Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile
      210              215              220
Phe Ile Phe Ile Thr Ile Met Arg Ile Arg Ser Ser Glu Gly Gln Leu
      225              230              235
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Thr Met Phe
      245              250              255
Tyr Gly Ser Leu Phe Cys Met Tyr Leu Arg Pro Thr Asn Glu Leu Ser
      260              265              270
Val Glu Gln Gly Lys Met Gly Val Val Phe Cys Ile Phe Val Ser Pro
      275              280              285
Met Leu Asn Pro Phe Ile Tyr Arg Leu Arg Asn Lys Asp Val Lys Gln
      290              295              300
Ala Leu Lys Arg Val Phe Met Arg Asn Leu
305              310

```

&lt;210&gt; 1513

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g430 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1513

```

Met Ser Leu Leu Phe Xaa Asp Xaa Asp Met Arg Asn Phe Thr Pro Leu
 1              5              10              15
Ser Gly Phe Ile Leu Gly Phe Thr Asp His Pro Glu Leu Gln Cys
      20              25              30
Leu Leu Phe Val Leu Phe Leu Leu Ile Tyr Met Phe Thr Val Val Gly
      35              40              45
Asn Leu Gly Met Ile Leu Leu Ile Lys Ile Asp Ser His Leu His Thr
      50              55              60
Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Leu Val Asp Phe Cys Tyr
      65              70              75              80
Ser Ser Val Ile Ala Pro Asn Met Leu Ile Asn Phe Trp Val Glu Asn
      85              90              95
Pro Val Ile Ser Phe Asn Glu Cys Ala Thr Gln Phe Phe Phe Phe Gly
      100              105              110
Ser Phe Ala Gly Ile Glu Gly Phe Leu Leu Ala Val Met Ala Tyr Asp
      115              120              125
Cys Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Val Leu Met Ser
      130              135              140
Pro His Leu Ser Ala Leu Leu Val Leu Ala Thr Tyr Leu Leu Gly Phe
      145              150              155              160
Val Asn Ala Ala Ile His Thr Gly Phe Thr Phe Gln Leu Ser Phe Cys
      165              170              175

```

His Ser Asn Ile Ile Asn Tyr Phe Phe Cys Asp Ile Pro Pro Leu Leu  
 180 185 190  
 Lys Leu Cys Ser Asp Thr His Ile Asn Glu Val Val Ile Phe Ala Phe  
 195 200 205  
 Ala Ser Phe Asn Glu Leu Ser Cys Leu Leu Leu Ile Leu Val Ser Cys  
 210 215 220  
 Leu Tyr Ile Leu Ala Ala Ile Leu Lys Ile His Ser Ala Glu Gly Arg  
 225 230 235 240  
 His Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile  
 245 250 255  
 Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Leu Arg Pro Ser Ser Ser  
 260 265 270  
 Tyr Ser Met Asp Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Val  
 275 280 285  
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val  
 290 295 300  
 Lys Ala Ser Leu Ser Lys Met Phe Lys Thr Val Ser Tyr Ile Ser Thr  
 305 310 315 320

&lt;210&gt; 1514

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g431 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1514

Met Gly Leu Pro Gly Ile His Glu Trp Gln His Trp Leu Ser Leu Pro  
 1 5 10 15  
 Leu Thr Leu Leu Tyr Leu Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile  
 20 25 30  
 Ile Thr Ile Gln His Glu Thr Val Leu His Glu Pro Met Tyr His Leu  
 35 40 45  
 Leu Gly Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met  
 50 55 60  
 Pro Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu  
 65 70 75 80  
 Pro Met Cys Phe Ala Gln Ile Tyr Ala Ile His Cys Phe Phe Cys Ile  
 85 90 95  
 Glu Ser Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Ile Ala Ile  
 100 105 110  
 Cys Arg Pro Leu Gln Tyr Pro Ser Ile Val Thr Lys Ala Phe Val Phe  
 115 120 125  
 Lys Ala Thr Gly Phe Ile Met Leu Arg Asn Gly Leu Leu Thr Ile Pro  
 130 135 140  
 Val Pro Ile Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile  
 145 150 155 160  
 Glu His Cys Leu Cys Ser Asn Leu Gly Val Ile Ser Leu Ala Cys Asp  
 165 170 175  
 Asp Ile Thr Val Asn Lys Phe Tyr Gln Leu Met Leu Ala Trp Val Leu  
 180 185 190  
 Val Gly Ser Asp Met Ala Leu Val Phe Ser Ser Tyr Ala Val Ile Leu  
 195 200 205  
 His Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Met Ser Lys Ala Leu  
 210 215 220  
 Ser Thr Cys Ser Ser His Leu Ile Leu Ile Leu Phe His Thr Gly Ile  
 225 230 235 240  
 Ile Val Leu Ser Val Thr His Leu Ala Glu Lys Lys Ile Pro Leu Ile  
 245 250 255  
 Pro Val Phe Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu Asn

```
<210> 1515
<211> 317
<212> PRT
<213> Unknown (H38g432 protein)
```

<220>  
<223> Synthetic construct

```
<210> 1516
<211> 317
<212> PRT
<213> Unknown (H38g433 protein)
```

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1516

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu  
 1 5 10 15  
 Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro  
 20 25 30  
 Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile  
 35 40 45  
 Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val  
 65 70 75 80  
 Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe  
 85 90 95  
 Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly  
 100 105 110  
 Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Ala Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly  
 130 135 140  
 Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro  
 145 150 155 160  
 Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val  
 165 170 175  
 Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala  
 180 185 190  
 Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met  
 195 200 205  
 Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu  
 210 215 220  
 Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro  
 245 250 255  
 Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln  
 260 265 270  
 His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met  
 275 280 285  
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly  
 290 295 300  
 Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys  
 305 310 315

&lt;210&gt; 1517

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g434 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1517

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

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<210> 1518
<211> 314
<212> PRT
<213> Unknown (H38g435 protein)
```

<220>  
<223> Synthetic construct

<400> 1518																
Met	Leu	Pro	Ser	Asn	Ile	Thr	Ser	Thr	His	Pro	Ala	Val	Phe	Leu	Leu	
1				5					10					15		
Val	Gly	Ile	Pro	Gly	Leu	Glu	His	Leu	His	Ala	Trp	Ile	Ser	Ile	Pro	
			20					25						30		
Phe	Cys	Phe	Ala	Tyr	Thr	Leu	Ala	Leu	Leu	Gly	Asn	Cys	Thr	Leu	Leu	
		35					40					45				
Phe	Ile	Ile	Arg	Ala	Asp	Ala	Ala	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe	
	50					55					60					
Leu	Ala	Met	Leu	Ala	Thr	Ile	Asp	Leu	Val	Leu	Ser	Ser	Thr	Thr	Leu	
65					70					75					80	
Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Asp	Gln	Glu	Ile	Asn	Phe	
				85					90					95		
Phe	Ala	Cys	Leu	Val	Gln	Met	Phe	Phe	Leu	His	Ser	Phe	Ser	Ile	Met	
			100					105					110			
Glu	Ser	Ala	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	
		115					120					125				
Cys	Lys	Pro	Leu	His	Tyr	Thr	Thr	Val	Leu	Thr	Gly	Ser	Leu	Ile	Thr	
	130					135					140					



Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile  
 165 170 175  
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly  
 180 185 190  
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser  
 195 200 205  
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu  
 210 215 220  
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro  
 245 250 255  
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro  
 260 265 270  
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met  
 275 280 285  
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr  
 290 295 300  
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met  
 305 310

&lt;210&gt; 1519

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g436 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu  
 35 40 45  
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr  
 100 105 110  
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu  
 130 135 140  
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr  
 145 150 155 160  
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His  
 165 170 175  
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile  
 195 200 205  
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala  
 210 215 220  
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

<210> 1520  
<211> 314  
<212> PRT  
<213> Unknown (H38g437 protein)

<220>  
<223> Synthetic construct

794

<210> 1521  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g438 protein)

<220>  
 <223> Synthetic construct

<400> 1521  
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu  
 1 5 10 15  
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu  
 35 40 45  
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu  
 50 55 60  
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro  
 65 70 75 80  
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe  
 85 90 95  
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu  
 100 105 110  
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys  
 130 135 140  
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu  
 145 150 155 160  
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala  
 165 170 175  
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn  
 180 185 190  
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly  
 195 200 205  
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln  
 210 215 220  
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly  
 225 230 235 240  
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser  
 245 250 255  
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His  
 260 265 270  
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val  
 290 295 300  
 Leu Gly Val Phe Pro Arg Lys Asp Val  
 305 310

<210> 1522  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g439 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1522

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1          5          10          15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
          20          25          30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
          35          40          45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
          65          70          75          80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
          85          90          95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
          100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
          130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
          145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
          165          170          175          180
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
          180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
          195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
          210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
          225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
          245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
          260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
          275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
          290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
          305          310          315

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&lt;210&gt; 1523

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g440 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
          20          25          30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
          35          40          45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60

```

Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly  
 85 90 95  
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr  
 100 105 110  
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu  
 130 135 140  
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser  
 145 150 155 160  
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His  
 165 170 175  
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr  
 180 185 190  
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu  
 195 200 205  
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala  
 210 215 220  
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val  
 245 250 255  
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys  
 260 265 270  
 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu  
 290 295 300  
 Val Ala Arg Val Phe Leu Ile Lys Lys  
 305 310

&lt;210&gt; 1524

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g441 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1524

Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe  
 20 25 30  
 Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val  
 35 40 45  
 Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly  
 85 90 95  
 Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

      115              120              125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130              135              140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145              150              155              160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165              170              175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180              185              190
Arg Ala Val Glu Met Leu Ala Phe Ala Phe Ala Val Leu Ile Val Leu
      195              200              205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
  210              215              220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225              230              235              240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245              250              255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
      260              265              270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
  290              295              300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305              310              315              320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325              330

```

&lt;210&gt; 1525

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g442 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1              5              10              15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20              25              30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35              40              45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50              55              60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
      65              70              75              80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85              90              95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100              105              110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115              120              125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130              135              140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
      145              150              155              160

```

Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val  
 165 170 175  
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val  
 180 185 190  
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser  
 195 200 205  
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys  
 210 215 220  
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro  
 225 230 235 240  
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr  
 245 250 255  
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn  
 260 265 270  
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu  
 275 280 285  
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu  
 290 295 300  
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu  
 305 310 315

&lt;210&gt; 1526

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g443 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(239)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val  
 1 5 10 15  
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr  
 20 25 30  
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr  
 35 40 45  
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr  
 50 55 60  
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu  
 65 70 75 80  
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His  
 85 90 95  
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu  
 100 105 110  
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu  
 115 120 125  
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met  
 130 135 140  
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His  
 145 150 155 160  
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile  
 165 170 175  
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln  
 180 185 190  
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys  
 195 200 205  
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

210 215 220  
 Arg Ile Leu Arg Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn  
 225 230 235

<210> 1527  
 <211> 255  
 <212> PRT  
 <213> Unknown (H38g444 protein)

<220>  
 <223> Synthetic construct

<400> 1527  
 Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile  
 1 5 10 15  
 Ser Thr Ile Val Pro Lys Met Ala Ser Asp Phe Leu His Gly Asn Lys  
 20 25 30  
 Ser Ile Ser Phe Thr Gly Cys Gly Ile His Ser Phe Phe Phe Thr Thr  
 35 40 45  
 Leu Ala Val Val Glu Ala Leu Leu Ile Ser Met Ala Tyr Val Arg  
 50 55 60  
 Cys Ile Ala Ile Cys Phe Pro Leu His Tyr Leu Met Arg Met Ser Lys  
 65 70 75 80  
 Arg Val Cys Val Leu Met Ile Thr Gly Ser Trp Ile Ile Gly Ser Ile  
 85 90 95  
 Asn Ala Cys Ala His Thr Val Tyr Ile Leu His Ile Pro Tyr Cys Pro  
 100 105 110  
 Ser Arg Val Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Val Thr  
 115 120 125  
 Leu Ala Cys Met Asp Thr Trp Val Tyr Glu Gly Thr Val Leu Leu Ser  
 130 135 140  
 Ala Thr Ile Phe Leu Val Phe Pro Phe Ile Ala Ile Ser Cys Ser Tyr  
 145 150 155 160  
 Gly Arg Val Leu Leu Ala Val Tyr His Met Lys Ser Ala Glu Gly Lys  
 165 170 175  
 Lys Lys Ala Tyr Leu Thr Cys Ser Thr His Leu Thr Val Val Thr Phe  
 180 185 190  
 Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg  
 195 200 205  
 Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr  
 210 215 220  
 Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Met  
 225 230 235 240  
 Gly Ala Leu Thr Arg Val Ile Gln Lys Ile Phe Ser Val Lys Ile  
 245 250 255

<210> 1528  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g445 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1528  
 Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly  
 1 5 10 15



Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu  
 20 25 30  
 Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Leu Ile  
 35 40 45  
 Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln  
 65 70 75 80  
 Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly  
 85 90 95  
 Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu  
 130 135 140  
 Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val  
 145 150 155 160  
 Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His  
 165 170 175  
 Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr  
 180 185 190  
 Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu  
 195 200 205  
 Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala  
 210 215 220  
 Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile  
 245 250 255  
 Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu  
 290 295 300  
 Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe  
 305 310 315 320

&lt;210&gt; 1529

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g446 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1529

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe  
 20 25 30  
 Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile  
 35 40 45  
 Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50 55 60  
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly  
 85 90 95  
 Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

	100		105		110
Leu	Leu	Leu	Thr	Ser	Met
		Ala	Tyr	Asp	Arg
				Tyr	Val
					Ala
					Ile
	115		120		125

<210> 1530  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g447 protein)

<220>  
 <223> Synthetic construct

<400> 1530

Met	Glu	Arg	Ala	Asn	Asp	Ser	Thr	Phe	Ser	Gly	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Asn	Arg	Pro	Gln	Leu	Glu	Thr	Ala	Leu	Phe	Val	Val	Ile	Leu
			20					25					30		
Ile	Ile	Tyr	Phe	Leu	Ser	Phe	Leu	Gly	Asn	Gly	Thr	Ile	Ile	Leu	Leu
		35					40					45			
Ser	Ile	Val	Asp	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55				60					
Asn	Leu	Ser	Phe	Met	Asp	Leu	Cys	Leu	Thr	Thr	Cys	Thr	Val	Pro	Gln
65					70					75					80
Thr	Leu	Val	Asn	Phe	Lys	Gly	Lys	Asp	Lys	Thr	Ile	Thr	Tyr	Gly	Gly
			85						90					95	
Cys	Val	Thr	Gln	Leu	Phe	Ile	Ala	Leu	Gly	Leu	Gly	Gly	Ser	Glu	Cys
			100					105					110		
Val	Leu	Leu	Ser	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg
		115					120					125			
Pro	Leu	His	Tyr	Met	Val	Ser	Met	His	Pro	Gln	Leu	Cys	Leu	Gln	Leu
	130					135						140			
Val	Val	Thr	Thr	Trp	Leu	Thr	Gly	Phe	Gly	Asn	Ser	Val	Ile	Gln	Thr
145					150					155					160
Ala	Leu	Thr	Met	Thr	Leu	Pro	Leu	Cys	Asp	Lys	Asn	Gln	Val	Asp	His
			165						170					175	
Phe	Phe	Cys	Glu	Val	Pro	Val	Met	Leu	Lys	Leu	Ser	Cys	Thr	Asn	Thr
		180					185						190		
Ser	Ile	Asn	Glu	Ala	Glu	Ile	Phe	Ala	Val	Ser	Val	Phe	Phe	Leu	Val
	195						200					205			
Val	Pro	Leu	Ser	Leu	Ile	Leu	Ala	Ser	Tyr	Gly	His	Ile	Thr	His	Ala
	210					215					220				
Val	Leu	Lys	Ile	Lys	Ser	Ala	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
225					230					235					240
Cys	Gly	Ser	His	Leu	Leu	Val	Val	Ile	Ile	Phe	Phe	Gly	Thr	Leu	Ile
			245						250					255	
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Gln	Asp	Val	Asn	Lys
		260						265					270		
Ser	Ile	Ala	Leu	Phe	Tyr	Thr	Leu	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu
		275					280						285		
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Thr	Lys	Lys	Thr
	290					295					300				
Ser	Gly	Glu	Asp	His	Arg	Cys	Met	Arg	Lys	Leu	Thr	Gln	Gly	Leu	Gln
305					310					315					320
Phe	Gln	Thr	Phe	Val	His										
				325											

<210> 1531  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g448 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1531

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe  
 20 25 30  
 Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile  
 35 40 45  
 Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50 55 60  
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys  
 85 90 95  
 Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu  
 100 105 110  
 Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro  
 115 120 125  
 Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile  
 130 135 140  
 Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val  
 145 150 155 160  
 Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe  
 165 170 175  
 Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp  
 180 185 190  
 Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe  
 195 200 205  
 Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val  
 210 215 220  
 Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys  
 225 230 235 240  
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr  
 245 250 255  
 Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val  
 260 265 270  
 Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser  
 290 295 300  
 Gln Arg Ile Cys Ser Val Lys Met  
 305 310

&lt;210&gt; 1532

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g449 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1532

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser  
 1 5 10 15  
 Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu  
 20 25 30  
 Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr  
 35 40 45  
 Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```

      50              55              60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys
65              70              75              80
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val
      85              90              95
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe
      100              105              110
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115              120              125
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu
      130              135              140
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser
145              150              155              160
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe
      165              170              175
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser
      180              185              190
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Gly Cys
      195              200              205
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu
      210              215              220
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile
225              230              235              240
Pro His Ile Leu Val Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val
      245              250              255
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu
      260              265              270
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr
      275              280              285
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys
      290              295              300
Arg Ile Phe Tyr Ser Glu Asn Val
305              310

```

&lt;210&gt; 1533

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g450 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1533

```

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile
1              5              10              15
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile
      20              25              30
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val
      35              40              45
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe
      50              55              60
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile
65              70              75              80
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser
      85              90              95
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly
      100              105              110
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala
      115              120              125
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys
      130              135              140

```

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala  
 145 150 155 160  
 His Ile Ser Tyr Met Pro His Ile Pro Val Cys Ser Ala Arg Ala Cys  
 165 170 175  
 Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr  
 180 185 190  
 Glu Cys Thr Val Phe Leu Ser Thr Thr Leu Phe Leu Met Phe Thr Phe  
 195 200 205  
 Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His  
 210 215 220  
 Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr  
 225 230 235 240  
 His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr  
 245 250 255  
 Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala  
 260 265 270  
 Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg  
 290 295 300  
 Ile Phe Pro Val Lys Met Lys  
 305 310

&lt;210&gt; 1534

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g451 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(192)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1534

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu  
 1 5 10 15  
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu  
 20 25 30  
 Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn  
 35 40 45  
 Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr  
 65 70 75 80  
 Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg  
 85 90 95  
 Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu  
 100 105 110  
 Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly  
 115 120 125  
 Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro  
 130 135 140  
 His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu  
 145 150 155 160  
 Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys  
 165 170 175  
 Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn  
 180 185 190

<210> 1535  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g452 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1535  
 Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly  
 1 5 10 15  
 Phe Ser Glu His Gln Glu Gln Ala Leu Leu Phe Gly Leu Phe Leu  
 20 25 30  
 Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn  
 100 105 110  
 Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser  
 115 120 125  
 His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu  
 130 135 140  
 Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His  
 145 150 155 160  
 Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro  
 165 170 175  
 His Phe Phe Cys Asp Leu Val Pro Leu Lys Leu Ala Cys Ser Ser  
 180 185 190  
 Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu  
 195 200 205  
 Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu  
 210 215 220  
 Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser  
 225 230 235 240  
 Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala  
 245 250 255  
 Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp  
 260 265 270  
 Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys  
 290 295 300  
 Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg  
 305 310 315

<210> 1536  
 <211> 252  
 <212> PRT  
 <213> Unknown (H38g453 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(252)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1536

```

His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
          20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
          35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
          50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
          65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
          85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
          100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
          115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
          130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
          145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
          165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Val Thr Tyr Trp Asp Ser Phe
          180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
          195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
          210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
          225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
          245          250

```

&lt;210&gt; 1537

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g454 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Phe Leu Phe Val Val Phe Phe
          20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
          35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
          50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
          65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
          85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

```

      100      105      110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Ala Lys
      115      120      125
Pro Leu His Tyr Val Thr Met Met Arg Lys Glu Val Trp Val Ala Leu
      130      135      140
Val Val Ala Ser Trp Val Ser Gly Gly Leu His Ser Ile Ile Gln Val
      145      150      155      160
Ile Leu Met Leu Pro Phe Pro Phe Cys Gly Pro Asn Thr Leu Asp Ala
      165      170      175
Phe Tyr Cys Tyr Val Leu Gln Val Val Lys Leu Ala Cys Thr Asp Thr
      180      185      190
Phe Ala Leu Glu Leu Phe Met Ile Ser Asn Asn Gly Leu Val Thr Leu
      195      200      205
Leu Trp Phe Leu Leu Leu Leu Gly Ser Tyr Thr Val Ile Leu Val Met
      210      215      220
Leu Arg Ser His Ser Gly Glu Gly Arg Asn Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ser His Met Leu Val Val Thr Leu His Phe Val Pro Cys Val Tyr
      245      250      255
Ile Tyr Cys Arg Pro Phe Met Thr Leu Pro Met Asp Thr Thr Ile Ser
      260      265      270
Ile Asn Asn Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser
      275      280      285
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Gln Arg Leu Gln Arg Arg
      290      295      300
Leu Gly Pro Ser Glu Ser Arg Lys Trp
      305      310

```

&lt;210&gt; 1538

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g455 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1538

```

Met Glu Arg Ile Asn His Thr Ser Ser Val Ser Glu Phe Ile Leu Leu
  1      5      10      15
Gly Leu Ser Ser Arg Pro Glu Asp Gln Lys Thr Leu Phe Val Leu Phe
      20      25      30
Leu Ile Val Tyr Leu Val Thr Ile Thr Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Arg Phe Asn Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr Thr Ser Val Val Pro
      65      70      75      80
Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala Leu Gly Asn Ser Asp
      100      105      110
Ser Cys Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
      115      120      125
Asp Pro Phe His Tyr Val Thr Thr Met Ser His His His Cys Val Leu
      130      135      140
Leu Val Ala Phe Ser Cys Ser Phe Pro His Leu His Ser Leu Leu His
      145      150      155      160
Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp Ser Asn Val Ile His
      165      170      175
His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys Leu Ser Cys Ser Ser
      180      185      190

```



Ile Phe Val Asn Glu Il Val Gln Met Thr Glu Ala Pro Ile Val Leu  
 195 200 205  
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr  
 210 215 220  
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile  
 245 250 255  
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His  
 260 265 270  
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu  
 290 295 300  
 Met Ser Lys Arg Ser  
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser  
 1 5 10 15  
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile  
 20 25 30  
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr  
 35 40 45  
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu  
 50 55 60  
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile  
 65 70 75 80  
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala  
 85 90 95  
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile  
 100 105 110  
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu  
 115 120 125  
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser  
 130 135 140  
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly  
 145 150 155 160  
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe  
 165 170 175  
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met  
 180 185 190  
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys  
 195 200 205  
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu  
 210 215 220  
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe  
 225 230 235 240  
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val  
 245 250 255  
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu  
 260 265 270  
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

```
<210> 1540
<211> 324
<212> PRT
<213> Unknown (H38q457 protein)
```

<220>  
<223> Synthetic construct

```
<210> 1541
<211> 314
<212> PRT
```

<213> Unknown (H38g458 protein)

<220>

<223> Synthetic construct

<400> 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
 1           5           10           15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
      20           25           30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
      35           40           45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
      50           55           60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
      65           70           75           80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
      85           90           95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
      100          105          110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
      115          120          125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
      130          135          140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
      145          150          155          160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
      165          170          175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
      180          185          190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
      195          200          205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
      210          215          220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
      225          230          235          240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
      245          250          255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
      260          265          270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
      275          280          285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
      290          295          300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
305          310

```

<210> 1542

<211> 307

<212> PRT

<213> Unknown (H38g459 protein)

<220>

<223> Synthetic construct

<400> 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1           5           10           15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
      20           25           30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

```

<400>	1543															
Met	Glu	Val	Ser	Gly	Asn	His	Thr	Ser	Val	Ala	Met	Phe	Val	Leu	Leu	
1				5					10					15		
Gly	Leu	Ser	Asp	Glu	Lys	Glu	Leu	Gln	Leu	Ile	Leu	Phe	Pro	Val	Phe	
			20					25					30			
Leu	Val	Ile	Tyr	Leu	Val	Thr	Leu	Ile	Trp	Asn	Met	Gly	Leu	Ile	Ile	
		35					40					45				
Leu	Ile	Arg	Ile	Asp	Ser	His	Leu	Asn	Thr	Pro	Met	Tyr	Phe	Phe	Leu	
	50					55					60					
Ser	Phe	Leu	Ser	Phe	Thr	Asp	Ile	Cys	Tyr	Ser	Ser	Thr	Ile	Ser	Pro	
65					70					75					80	
Arg	Met	Leu	Ser	Asp	Phe	Leu	Lys	Asp	Lys	Lys	Thr	Ile	Ser	Phe	Leu	
				85					90					95		
Ala	Cys	Ala	Thr	Gln	Tyr	Phe	Leu	Gly	Ala	Trp	Met	Ser	Leu	Ala	Glu	
			100					105					110			
Cys	Cys	Leu	Leu	Val	Ile	Met	Ala	Cys	Asp	Arg	Tyr	Val	Ala	Ile	Gly	
		115					120					125				

Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys  
 130 135 140  
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His  
 145 150 155 160  
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln  
 165 170 175  
 His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn  
 180 185 190  
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly  
 195 200 205  
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala  
 210 215 220  
 Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala  
 245 250 255  
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys  
 260 265 270

&lt;210&gt; 1544

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g461 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1544

Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys  
 1 5 10 15  
 Cys Gly Xaa His Asn Lys Ile Thr Phe Phe Leu Phe Ile Leu Leu Glu  
 20 25 30  
 Phe Thr Glu Asp Leu Gly Leu Gln Val Leu Phe Phe Ile Phe Leu  
 35 40 45  
 Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu  
 50 55 60  
 Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly  
 65 70 75 80  
 Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp  
 85 90 95  
 Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly  
 100 105 110  
 Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr  
 115 120 125  
 Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro  
 130 135 140  
 Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val  
 145 150 155 160  
 Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser  
 165 170 175  
 Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe  
 180 185 190  
 Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu  
 195 200 205  
 Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro  
 210 215 220  
 Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

```

225          230          235          240
Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly
                245          250          255
Ser Pro Leu Thr Ala Leu Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile
                260          265          270
Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly
                275          280          285
Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
                290          295          300
Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp
305          310          315          320
Arg Leu Gln Phe Leu Lys Glu Lys Tyr
                325

```

&lt;210&gt; 1545

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g462 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(349)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1545

```

Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
 1          5          10          15
Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu
                20          25          30
Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile
                35          40          45
His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
                50          55          60
Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys
                85          90          95
Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe
                100          105          110
Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro
                115          120          125
Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val
                130          135          140
Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro
145          150          155          160
Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe
                165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
                180          185          190
Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile
                195          200          205
Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val
                210          215          220
Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys
225          230          235          240
Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
                245          250          255
Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala
                260          265          270

```

Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val  
 290 295 300  
 Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala  
 305 310 315 320  
 Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala  
 325 330 335  
 Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro  
 340 345

<210> 1546

<211> 319

<212> PRT

<213> Unknown (H38g463 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1546

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly  
 1 5 10 15  
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala  
 20 25 30  
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala  
 35 40 45  
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala  
 50 55 60  
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg  
 85 90 95  
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys  
 100 105 110  
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser  
 115 120 125  
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val  
 130 135 140  
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu His Val  
 145 150 155 160  
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln  
 165 170 175  
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met  
 180 185 190  
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile  
 195 200 205  
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr  
 245 250 255  
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala  
 260 265 270  
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val  
 275 280 285  
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

290 295 300  
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr  
 305 310 315

<210> 1547  
 <211> 280  
 <212> PRT  
 <213> Unknown (H38g464 protein)

<220>  
 <223> Synthetic construct

<400> 1547  
 Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu Ile  
 1 5 10 15  
 Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser His  
 20 25 30  
 Leu Ala Leu Thr Tyr Phe Ser Phe Ser Ser Val Thr Val Pro Lys Met  
 35 40 45  
 Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys  
 50 55 60  
 Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe  
 65 70 75 80  
 Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro  
 85 90 95  
 Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val  
 100 105 110  
 Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu  
 115 120 125  
 Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val  
 130 135 140  
 Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe  
 145 150 155 160  
 Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu  
 165 170 175  
 Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile  
 180 185 190  
 Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys  
 195 200 205  
 Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly  
 210 215 220  
 Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile  
 225 230 235 240  
 Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile  
 245 250 255  
 Tyr Ser Ile Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe  
 260 265 270  
 Ser Arg Ala Thr Phe Phe Ser Trp  
 275 280

<210> 1548  
 <211> 303  
 <212> PRT  
 <213> Unknown (H38g465 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(303)  
 <223> Xaa = Any Amino Acid



<400> 1548  
 Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn  
 1 5 10 15  
 Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro  
 20 25 30  
 Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu  
 35 40 45  
 Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala  
 50 55 60  
 Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu  
 65 70 75 80  
 Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu  
 85 90 95  
 Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu  
 100 105 110  
 Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val  
 115 120 125  
 Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr  
 130 135 140  
 Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys  
 145 150 155 160  
 Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln  
 165 170 175  
 Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val  
 180 185 190  
 Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala  
 195 200 205  
 Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile  
 210 215 220  
 Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg  
 225 230 235 240  
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu  
 245 250 255  
 Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu  
 260 265 270  
 Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe  
 275 280 285  
 Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu  
 290 295 300

<210> 1549

<211> 309

<212> PRT

<213> Unknown (H38g466 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1549

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

```

      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

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&lt;210&gt; 1550

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g467 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```

Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser  
 145 150 155 160  
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly  
 165 170 175  
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala  
 195 200 205  
 Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala  
 210 215 220  
 Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr  
 225 230 235 240  
 Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser  
 245 250 255  
 Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu  
 290 295 300  
 Leu Gly Lys Gly Arg Glu Val Gly  
 305 310

<210> 1551  
 <211> 82  
 <212> PRT  
 <213> Unknown (H38g468 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(82)  
 <223> Xaa = Any Amino Acid

<400> 1551  
 Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala  
 1 5 10 15  
 Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg  
 20 25 30  
 Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val  
 35 40 45  
 Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile  
 50 55 60  
 Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg  
 65 70 75 80  
 Lys Thr

<210> 1552  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g469 protein)

<220>  
 <223> Synthetic construct

<400> 1552  
 Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu

```
<210> 1553
<211> 318
<212> PRT
<213> Unknown (H38g470 protein)
```

<220>  
<223> Synthetic construct

<400> 1553																
Met	Pro	Thr	Val	Asn	His	Ser	Gly	Thr	Ser	His	Thr	Val	Phe	His	Leu	
1				5					10					15		
Leu	Gly	Ile	Pro	Gly	Leu	Gln	Asp	Gln	His	Met	Trp	Ile	Ser	Ile	Pro	
			20					25					30			
Phe	Phe	Ile	Ser	Tyr	Val	Thr	Ala	Leu	Leu	Gly	Asn	Ser	Leu	Leu	Ile	
		35					40					45				
Phe	Ile	Ile	Leu	Thr	Lys	Arg	Ser	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe	
	50					55					60					
Leu	Cys	Met	Leu	Ala	Gly	Ala	Asp	Ile	Val	Leu	Ser	Thr	Cys	Thr	Ile	
65				70					75					80		
Pro	Gln	Ala	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Ala	Gly	Asp	Ile	Ser	Leu	
				85					90					95		
Asp	Arg	Cys	Ile	Thr	Gln	Leu	Phe	Phe	Ile	His	Ser	Thr	Phe	Ile	Ser	
			100					105					110			

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile  
           115                          120                          125  
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys  
           130                          135                          140  
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro  
 145                          150                          155                          160  
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile  
           165                          170                          175  
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn  
           180                          185                          190  
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr  
           195                          200                          205  
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu  
           210                          215                          220  
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu  
 225                          230                          235                          240  
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser  
           245                          250                          255  
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro  
           260                          265                          270  
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met  
           275                          280                          285  
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln  
           290                          295                          300  
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val  
 305                          310                          315

&lt;210&gt; 1554

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g471 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu  
   1                          5                          10                          15  
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe  
           20                          25                          30  
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala  
           35                          40                          45  
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu  
           50                          55                          60  
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro  
 65                          70                          75                          80  
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala  
           85                          90                          95  
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp  
           100                          105                          110  
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg  
           115                          120                          125  
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala  
           130                          135                          140  
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr  
 145                          150                          155                          160  
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro  
           165                          170                          175  
 His Phe Phe Cys Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp  
           180                          185                          190  
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

```

      195              200              205
Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala
  210              215              220
Ala Val Leu Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val
      245              250              255
Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly
      260              265              270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala
      290              295              300
Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser
  305              310

```

&lt;210&gt; 1555

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g472 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1555

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
      20              25              30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
      35              40              45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
      50              55              60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
      65              70              75              80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
      85              90              95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
      100              105              110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
      115              120              125
Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
      130              135              140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
      145              150              155              160
Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
      165              170              175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
      180              185              190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
      195              200              205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
      210              215              220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
      225              230              235              240
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
      245              250              255

```

Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp  
 260 265 270  
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro  
 275 280 285  
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg  
 290 295 300  
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile  
 305 310 315

<210> 1556

<211> 320

<212> PRT

<213> Unknown (H38g473 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1556

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
 20 25 30  
 Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly  
 195 200 205  
 Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210 215 220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly  
 245 250 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly  
 260 265 270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
 290 295 300  
 Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

<210>	1558
<211>	330
<212>	PRT